GenCore version 5.1.7

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 3, 2006, 15:25:40 ; Search time 316 Seconds
(without alignments)
3617.000 Million cell updates/sec

Title: US-10-736-868-2
Perfect score: 3291
Sequence: 1 MILFLFLFLLLGFCIAPLSA.....SKTKRFVGGNGAFDMPALGL 643

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	171	5.2	100990	3	US-09-409-800B-2	Sequence 2, Appli
2	169.5	5.2	6151	3	US-09-799-451-528	Sequence 528, App
3	162.5	4.9	5883	3	US-09-949-016-5001	Sequence 5001, Ap
4	159	4.8	2680	2	US-08-533-306A-5	Sequence 5, Appli
5	159	4.8	2680	2	US-08-742-923A-5	Sequence 5, Appli
6	159	4.8	2887	2	US-08-533-306A-3	Sequence 3, Appli
7	159	4.8	2887	2	US-08-742-923A-3	Sequence 3, Appli
8	159	4.8	4935	3	US-09-949-016-1019	Sequence 1019, Ap
9	159	4.8	4935	3	US-09-949-016-5054	Sequence 5054, Ap
10	159	4.8	5574	3	US-09-917-254-40	Sequence 40, Appl
11	159	4.8	6861	3	US-09-949-016-1240	Sequence 1240, Ap
12	159	4.8	6861	3	US-09-949-016-1241	Sequence 1241, Ap
13	159	4.8	6861	3	US-09-949-016-1242	Sequence 1242, Ap
c 14	158.5	4.8	19269	3	US-09-902-540-1175	Sequence 1175, Ap
15	157	4.8	6175	3	US-08-875-435B-1	Sequence 1, Appli
16	157	4.8	6856	3	US-09-566-921-42	Sequence 42, Appl
17	156	4.7	3807	3	US-09-645-456A-8	Sequence 8, Appli
18	156	4.7	3807	3	US-09-425-324A-8	Sequence 8, Appli
19	156	4.7	3807	3	US-09-645-791-8	Sequence 8, Appli
20	155.5	4.7	3972	3	US-09-645-456A-6	Sequence 6, Appli
21	155.5	4.7	3972	3	US-09-425-324A-6	Sequence 6, Appli
22	155.5	4.7	3972	3	US-09-645-791-6	Sequence 6, Appli
23	153.5	4.7	6396	3	US-09-949-016-3344	Sequence 3344, Ap
24	153	4.6	9551	2	US-08-056-200-93	Sequence 93, Appl
25	153	4.6	9551	2	US-08-800-644-93	Sequence 93, Appl
c 26	152.5	4.6	1761	3	US-09-252-991A-16401	Sequence 16401, A
27	152.5	4.6	3489	3	US-09-252-991A-16193	Sequence 16193, A
28	152.5	4.6	4055	3	US-09-688-188B-10	Sequence 10, Appl
29	152.5	4.6	4055	3	US-09-291-417D-10	Sequence 10, Appl
30	152	4.6	3831	3	US-09-645-456A-5	Sequence 5, Appli
31	152	4.6	3831	3	US-09-425-324A-5	Sequence 5, Appli
32	152	4.6	3831	3	US-09-645-791-5	Sequence 5, Appli
33	151.5	4.6	3996	3	US-09-645-456A-2	Sequence 2, Appli
34	151.5	4.6	3996	3	US-09-425-324A-2	Sequence 2, Appli
35	151.5	4.6	3996	3	US-09-645-791-2	Sequence 2, Appli
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37	150.5	4.6	3228	3	US-09-252-991A-1816	Sequence 1816, Ap
c 38	150.5	4.6	3546	3	US-09-252-991A-2143	Sequence 2143, Ap
39	150.5	4.6	4209	3	US-09-248-796A-400	Sequence 400, App
40	150.5	4.6	7596	3	US-09-023-655-1463	Sequence 1463, Ap
41	149	4.5	2130	3	US-09-248-796A-4942	Sequence 4942, Ap
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43	146.5	4.5	3894	3	US-09-645-456A-7	Sequence 7, Appli
44	146.5	4.5	3894	3	US-09-425-324A-7	Sequence 7, Appli
45	146.5	4.5	3894	3	US-09-645-791-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-409-800B-2
; Sequence 2, Application US/09409800B
; Patent No. 6706522
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Valerie
; APPLICANT: Rose, Debra J.
; APPLICANT: Mayhew, George F.
; APPLICANT: Perna, Nicole
; APPLICANT: Perry, Robert D.
; APPLICANT: Straley, Susan C.
; APPLICANT: Fetherston, Jacqueline D.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Plano, Gregory V.
; TITLE OF INVENTION: Plasmid DNA From Yersinia Pestis
; FILE REFERENCE: 960296.95939
; CURRENT APPLICATION NUMBER: US/09/409,800B
; CURRENT FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 100990
; TYPE: DNA
; ORGANISM: Yersinia pestis
US-09-409-800B-2

Alignment Scores:

Pred. No.:	5.04e-05	Length:	100990
Score:	171.00	Matches:	142
Percent Similarity:	34.0%	Conservative:	100
Best Local Similarity:	19.9%	Mismatches:	260
Query Match:	5.2%	Indels:	210

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Qy        36 LeuValGly---------------------------------------------------- 38
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Qy        39 ---------LysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGluLeu 55
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Db     85345 ATGAAGATGCGCGAGAGAGGAAAGGCTCCGTCTACCGGGCTTTGGAACGCGCTGGAA--- 85401

Qy        56 MetGlyValGlnPheValAspAlaLeuIleLysLysGlyGlnMetGluMetAlaLysGly 75
                          |||     |||::::::       ::::::      |||
Db     85402 -----------------GACGTTTTTATTGAACGCAGAATGGGACAGGTATTCAACGGA 85443

Qy        76 AlaPheLysThrGlnLeuGluValLeuGluLysValHisProAspGlnPheAspLysTyr 95
                :::      |||                |||              |||||||||
Db     85444 ACCCGTCGTAATTTGCTAGCCACACAGAACCTGGTG-----------ATCGACAAATAC 85491

Qy        96 LysLysLeuLysValAspAspLeuAlaAlaAspAlaValMetGlnGlnAlaGluMet---- 114
                |||   ||||||  :::      :::                |||   |||:::
Db     85492 TTCAAGGGCAAAGTGTCAGAGGCGGTTTCAATCTGCCACGGCAACCAGCGTGAATTGTTC 85551

Qy       115 -----------------AlaLysLeuGlnProLysSerGlyAsnAla---PheIleAsp 127
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Db     85552 CTGAAATTCTTCCTTTGCCCGGTCGTCCGCGCCTGGGATGGCCAAAGCCCTTTCATCGAC 85611

Qy       128 MetLeuAsnGlyAsnGlyIleProIleGlySerSerIle---------------ArgGly 142
                :::      :::         |||         :::                  |||
Db     85612 TTTATGGAAGAACACTGGCACCTCATCGATAAGCCTGTAGCCTTGCTCAAAGAGCATGGT 85671

Qy       143 LeuGluAspAlaIleArgThrGlnArgAspMetGluAsnThrAspProSerGluGlnIle 162
             ::::::   |||:::      |||:::|||   ||||||:::         ::::::
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             |||   |||:::          |||
Db     85723 GCAGCTGCTATCGCCCAAATCATGCAGGAT---------------------------- 85752

Qy       183 IleAlaGlyLysAsnProPheLysMetProGlnGlnMetArgLysAlaGlnAlaAlaPro 202
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Qy       203 SerSerValPheGlnGlnAlaLeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProVal 222
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Qy       243 GlnArgGluLeuGlnGluGluAsp---GluAspAspAspAspLeuGluAspGluAspVal 261
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Db     85906 GACAAGGAAGAGCAAGAAGATGATGCCTCAGAAGAGGAAGATTCTGGGGATTCTGATTTG 85965

Qy       262 ProArgArgArgSerSerAspGlyGluProGlnSerGluAlaGluHisGlnArgArgAsp 281
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Db     85966 CCT--------------GATTCATTAGATAAGGACTTACCTATACATGAT--------- 86001

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Db     86002 --------------------------------AAAGAAATTAGTGATACAGAAAGTAAA 86028

Qy       302 GlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgProLeu 321
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Qy       322 AlaMetAsnAsp---GluAspGluSerAlaPheArgAlaMetGluAla------------ 336
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Qy       354 GlyGluSerAsp-----------------------------------AspAspGluAsp 361
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Qy       362 GluGluAspGluAsnLeuIleAspProSerGluAsnSerPheArg--------------- 376
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Db     86269 GAAGGCGAAGAGGACGTCGCCGATCACACTGACGGCGAAGGCAAGGAAAATGAGGATGCC 86328

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Db     86329 GCGGAAGCGCCTGAAGACAGTGAGTCAGGCTTTGTTCCTGCGCCGGATGAAATGACTCTG 86388

Qy       393 AsnAspGluLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAspVal------ 410
             |||   ||||||   |||||||||   ::::::        ||::::::
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Qy       411 -----------------------GluLysTyrLeuAlaProLysProMetGluPheAsn 422
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Db     86446 GACGCACTGTCGGCCACCATCAGCAAAGAGCTTATGAGCGCCTCACTTTCTGAGTATCGC 86505

Qy       423 ProLysProGlnProGlyTyrPheAlaProArgLysIleProThrArgProArgLysMet 442
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Qy       443 LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIleArgArg--------- 459
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Db     86530 ------------ATCGGGTTGATTGATGAGGCTGAAGAGCATGTAAAACGCACCAGAAAG 86577

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Qy       487 PheMetAspAspLysLeuGluAsnThrLeuLysGlyArg---------GlnMetLeuThr 503
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Db     86698 GCCAAAGAC------CTGGAGCGAGCTATCGCCAGCCGCAACCGAGTTCAGTTCATACCG 86751

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Db     86752 GGTCAGAGACGTGGG-------------------------------CGGATACATGGC 86778

Qy       524 AlaProThrAlaLysAlaGluMetIleAspAlaLysValPheGlnAspIleGluGlu--- 542
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Db     86779 GCGAACCTGTATCGTCTGGCAATGAACGACGACCGCGTGTTCCGCAAGAAAGAAGACCAC 86838

Qy       543 --------------------ArgProIleProProLeuPhePheGluProLysGlyArg 555
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Db     86839 AGAGCGGTGAACGCGTGCGTCCAGCAGGTGATCGACTTGTCCGGCTCAATGGGCGGCAGG 86898

Qy       556 HisThrArgLeuArgTrpThrGlyAlaAsnGluLysGluIleProGlyLeuGlySerArg 575
                :::|||                                      |||   |||
Db     86899 AAGATTCAACTG--------------------------------GCACTCGCCAGCGCC 86925

Qy       576 Phe---IleLeuProSerLeuAspPro---ThrMetProAlaLeuAsnThrAlaPheSer 593
             :::   |||      :::||||||          :::|||   :::   |||   |||:::
Db     86926 TACACCATTGCGGATGCTCTGGATCGTATCAATGTGCCTAACATCATCACCGGCTTTACA 86985

Qy       594 ThrGlnGlyArgAlaArgAspGluTrpAspThrMetPheLys------------------ 607
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Db     86986 ACGTTTGGT------AGCCCAGATTATGAAACCATGTCGAAGCGCGGGTTTACACGTTTC 87039

Qy       608 ------------------IleProAsnAsnTrpAsn 613
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Db      87040 GAGGCGCTCATGCTGCCCATTATCAAAAACTGGAAT 87075

RESULT 2
US-09-799-451-528
; Sequence 528, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Goodrich, Ryle
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Yamazaki, Victoria
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Ghosh, Reena
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 6783969el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 803
;  CURRENT APPLICATION NUMBER: US/09/799,451
;  CURRENT FILING DATE:  2001-03-05
;  NUMBER OF SEQ ID NOS: 948
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 528
;   LENGTH: 6151
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (263)..(3133)
US-09-799-451-528

Alignment Scores:
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Score:                  169.50        Matches:         118
Percent Similarity:     36.3%         Conservative:    108
Best Local Similarity:  18.9%         Mismatches:      248
Query Match:            5.2%          Indels:          149
DB:                     3             Gaps:            22

US-10-736-868-2 (1-643) x US-09-799-451-528 (1-6151)

Qy         36 LeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGluLeu 55
Db        632 CTGACTGGCTCATCCCATCATCACCACCACCAGGTCCCCTCCATG---TTGAGGCAGGTA 688

Qy         56 MetGlyValGlnPheValAspAlaLeuIleLysLysGlyGlnMetGluMetAlaLysGly 75
Db        689 AGAGACAGCACAATGTTAGATCTTCAGGCCCAGCTGAAAGAACTGCAGAGAGAGAATGAC 748

Qy         76 AlaPheLysThrGlnLeuGluValLeuGluLysValHisProAspGlnPheAspLysTyr 95
Db        749 CTCCTCCGGAAAGAGCTAGACATCAAGGACAGCAAATTGGGATCTTCCATGAACAGTATT 808

Qy         96 LysLysLeuLysValAspAspLeuAlaAlaAspAlaValMetGlnGlnAlaGluMetAla 115
Db        809 AAGACTTTCTGGAGTCCTGAGCTTAAGAAGGAGAGAGTCTTGAGGAAAGAAGAGGCAGCG 868

Qy        116 LysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsnGlyIlePro 135
Db        869 CGGATGTCTGTCCTCAAGGAGCAGATGAGGGTTTCCCATGAAGAAAATCAGCACCTACAG 928

Qy        136 IleGlySerSerIleArgGlyLeuGluAspAlaIleArgThrGlnArgAspMetGluAsn 155

Db        929 TTG------ACAATCCAGGCCCTTCAAGATGAGCTGCGAACCCAGAGAGACCTCAACCAC 982

Qy        156 ThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPheGlnThrGlnIleLeu 175
Db        983 CTCCTCCAGCAAGAGAGTGGCAACCGAGGAGCG---GAGCACTTCACCATCGAGCTGACC 1039

Qy        176 ProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPheLysMetProGlnGlnMet 195
Db       1040 ----------------------------GAGGAGAACTTTAGGCGGCTCCAAGCCGAG 1069

Qy        196 ArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAlaLeuAlaGlnArgAlaMet 215
Db       1070 CATGACAGGCAGGCTAAGGAGCTGTTCCTTTTGAGGAAGACATTAGAGGAAATGGAGCTG 1129

Qy        216 LeuGlyLysAsnAlaProValAlaGlyGlyArgGlyGluGluGlnArgMetMetMetAsn 235
Db       1130 ----------------------------AGAATTGAAACGCAGAAACAAACCCTCAAT 1159

Qy        236 ArgValAspGlnArgMetGlnGln------ArgGluLeuGlnGluGluAspGluAspAsp 253
Db       1160 GCCCGAGATGAGTCAATTAAAAAACTTCTTGAGATGTTGCAAAGTAAAGGCTTGCCATCC 1219

Qy        254 AspAspLeuGluAspGluAspValProArgArgArgSerSerAspGlyGluProGln--- 272
Db       1220 AAAAGCCTGGAGGATGACAATGAGCGAACGCGGCGGATGGCAGAGGCTGAGTCTCAGGTC 1279

Qy        273 --------------------------------SerGluAlaGluHisGlnArgArgAsp 281
Db       1280 AGCCACTTGGAAGTGATTTTAGATCAGAAAGAGAAGGAAAACATACATCTTAGAGAGGAA 1339

Qy        282 LeuAlaArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsnAlaGluVal 301
Db       1340 TTGCACCGAAGAAGCCAACTTCAGCCG----------------GAGCCAGCCAAGACG 1381

Qy        302 GlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgProLeu 321
Db       1382 AAGGCTCTCCAGACTGTCATCGAAATGAAGGACACAAAAATCGCTTCA---------TTG 1432

Qy        322 AlaMetAsnAspGluAsp---GluSerAlaPheArgAlaMetGluAlaArgAlaLysLeu 340
Db       1433 GAACGAAACATAAGGGATCTTGAGGATGAGATCCAGATGTTAAAAGCCAATGGTGTGCTG 1492

Qy        341 AspGlnLysSerGlnLeuValLeuGlyLeuHisGlyPheGlyGluSerAspAspAspGlu 360
Db       1493 ------------------------------------------------AACACTGAG 1501

Qy        361 AspGluGluAspGluAsnLeuIleAspProSerGluAsnSerPheArgArgAlaProLeu 380
Db       1502 GACCGCGAAGAAGAG---------------------------------------------- 1516

Qy        381 ArgLeuSerSerGlyPheValGluLysLeuLysSerAsnAspGluLeuLysSerAlaLeu 400
Db       1517 -------------------------ATCAAACAAATTGAGGTTTACAAAAGTCACTCC 1549

Qy        401 AspArgIleLysTyrArgValAspAspValGluLysTyrLeuAlaProLysProMetGlu 420
Db       1550 AAGTTTATGAAGACCAAGATTGATCAGCTGAAGCAGGAACTTTCAAAGAAAGAGTCGGAA 1609

Qy        421 PheAsnProLysProGlnProGlyTyrPheAlaProArgLysIleProThrArgProArg 440
Db       1610 CTT--------------------CTTGCCTTACAAACAAAGCTTGAAACCCTCAGCAAT 1648

Qy        441 LysMetLeuProLeuLeuIleGlySerAspProLysValGlnGluGluIleArgArgHis 460
Db       1649 CAA-----------------AATTCAGATTGCAAGCAACACATTGAAGTGCTCAAAGAG 1690

Qy        461 ProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeuLysAsnAsn 480
Db       1691 TCACTTACT-----------GCCAAAGAACAGAGGGCTGCCATC---CTTCAGACTGAG 1735

Qy        481 ProSerLeuAlaAlaLeuPheMetAspAspLys---------LeuGluAsnThrLeuLys 497
Db       1736 GTAGATGCGCTGAGATTACGACTGGAAGAAAAAGAATCTTTCCTCAATAAAAAAACAAAA 1795
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Qy       498 GlyArgGlnMetLeuThrAspGluGlnLysGlyArgThrArgValLysThrIleArgAla 517
Db      1796 CAGCTACAGGACCTCACA---GAAGAGAAGGGG-------------------------- 1825

Qy       518 LeuProArgLeuPheGlyAlaProThrAlaLysAlaGluMetIleAspAlaLysValPhe 537
Db      1826 ------------------------ACACTGGCCGGTGAAATTCGTGACATGAAAGATATG 1861

Qy       538 GlnAspIleGluGluArgProIleProProLeuPhePheGluProLysGlyArgHisThr 557
Db      1862 TTAGAAGTGAAGGAAAGAAAAATCAATGTTCTTCAGAAAAAGATTGAAAACTTGCAAGAA 1921

Qy       558 ArgLeuArgTrpThrGlyAlaAsnGluLysGluIleProGlyLeuGlySerArgPheIle 577
Db      1922 CAACTTAGG---------GATAAAGACAAGCAACTGACCAACCTGAAAGACAGA------ 1966

Qy       578 LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSerThr--------- 594
Db      1967 GTGAAGTCCTTGCAGACGGATTCCAGTAATACAGATACTGCACTGGCGACGCTAGAGGAA 2026

Qy       595 -------------------------------------GlnGlyArgAlaArgAspGlu 601
Db      2027 GCTCTGTCAGAGAAGGAGAGAATAATTGAGCGCTTGAAAGAACAGCGAGAAAGAGATGAT 2086

Qy       602 TrpAspThrMetPheLysIleProAsnAsnTrpAsnProGlyAspGluValGlyPheLys 621
Db      2087 CGGGAAAGACTAGAAGAGATAGAATCCTTCCGAAAAGAGAACAAAGACCTGAAAGAGAAG 2146

Qy       622 MetAsnSer 624
Db      2147 GTCAATGCT 2155
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RESULT 3
US-09-949-016-5001
; Sequence 5001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5001
; LENGTH: 5883
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5001

Alignment Scores:

Pred. No.:	4.54e-06	Length:	5883
Score:	162.50	Matches:	136
Percent Similarity:	35.9%	Conservative:	88
Best Local Similarity:	21.8%	Mismatches:	213
Query Match:	4.9%	Indels:	192
DB:	3	Gaps:	25

US-10-736-868-2 (1-643) x US-09-949-016-5001 (1-5883)

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Qy        12 GlyPheCysIleAlaProLeuSer------AlaGlnSerProSerThrSerAsp------ 27
Db      3860 GGCTTCTCAGCCAGTCCGACAGCAAGTCCAGCAAGCTCACCAAGGACTTCTCCGCGCTGG 3919

Qy        28 AlaProGly------AlaLeuLeuSerSerLeuValGlyLysSerHisGlnLysLeuPro 45
Db      3920 AGTCCCAGCTGCAGGACACTCAGGAGCTG-CTGCAGGAGGAGAACCGGCAGAAGCTGAGC 3978

Qy        46 LeuAlaProSerMetGluAlaLeuGlu------------------------------- 54
Db      3979 CTGAGCACCAAGCTCAAGCAGGTGGAGGACGAGAAGAATTCCTTCCGGGAGCAGCTGGAG 4038

Qy        55 ----------------------------------------LeuMetGlyValGlnPhe 60
Db      4039 GAGGAGGAGGAGGCCAAGCACAACCTGGAGAAGCAGATCGCCACCCTCCATGCCCAGGTG 4098

Qy        61 ValAspAlaLeuIleLysLysGlyGlnMetGluMetAlaLysGlyAlaPheLysThrGln 80
Db      4099 GCCGAC---------ATGAAAAAGAAGATGGAGGACAGTGTGGGGTGCCTGGAAACTGCT 4149

Qy        81 LeuGluValLeuGluLysValHisProAsp------------------------------ 90
Db      4150 GAGGAGGTGAAGAGGAAGCTCCAGAAGGACCTGGAGGGCCTGAGCCAGCGGCACGAGGAG 4209

Qy        91 ---------GlnPheAspLysTyrLysLysLeuLys------------------ValAsp 101
Db      4210 AAGGTGGCCGCCTACGACAAGCTGGAGAAGACCAAGACGCGGCTGCAGCAGGAGCTGGAC 4269

Qy       102 AspLeuAlaAlaAspAlaValMetGlnGlnAlaGluMetAlaLysLeuGlnProLysSer 121
Db      4270 GACCTGCTGGTGGACCTGGACCACCAGCGCCAGAGCGCGTGCAACCTGGAGAAGAAGCAG 4329

Qy       122 GlyAsnAlaPheIleAspMetLeuAsnGlyAsnGlyIleProIleGly------------ 137
Db      4330 AAGAAG------TTTGACCAGCTCCTGGCGGAGGAGAAGACCATCTCTGCCAAGTATGCA 4383

Qy       138 ------------------------------------------------------SerSer 139
Db      4384 GAGGAGCGCGACCGGGCTGAGGCGGAGGCCCGAGAGAAGGAGACCAAGGCTCTGTCGCTG 4443

Qy       140 IleArgGlyLeuGluAspAlaIleArgThrGlnArgAspMetGluAsnThrAspProSer 159
Db      4444 GCCCGGGCCCTGGAGGAAGCCATGGAGCAGAAGGCGGAGCTGGAGCGGCTCAAC------ 4497

Qy       160 GluGlnIleAlaLysAlaValMetAspLysPheGlnThrGlnIleLeuProGlyLeuVal 179
Db      4498 ------------------------AAGCAGTTCCGCACGGAG---------------ATG 4518

Qy       180 AlaAsnMetIleAlaGlyLysAsnProPhe---LysMetProGlnGlnMetArgLysAla 198
Db      4519 GAGGACCTTATGAGCTCCAAGGATGATGTGGGCAAGAGTGTCCACGAGCTGGAGAAGTC- 4577

Qy       199 GlnAlaAlaProSerSerValPheGlnGlnAlaLeuAlaGlnArgAlaMetLeuGlyLys 218
Db      4578 CAAGCGGGCCCT----------------------------AGAGCAGCAGGTGGAGGA 4607

Qy       219 Asn---------AlaProValAlaGlyGlyArgGlyGluGluGlnArgMetMetMetAsn 235
Db      4608 GATGAAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAGGCCACCGAAGATGCCAAGCT 4667

Qy       236 -ArgValAspGlnArgMetGln------------------GlnArgGluLeuGlnGluGl 249
Db      4668 GCGGTTGGAGGTCAACCTGCAGGCCATGAAGGCCCAGTTCGAGCGGGACCTGCAGGGCCG 4727

Qy       249 uAspGluAspAspAspAspLeuGluAspGluAspValProArgArgArgSerSerAspGl 269
Db      4728 GGACGAGCAGAGCGAGGAGAAGAAGAAGCAGCTGGTCAGACAGGTGCGGGAGATGGAGGC 4787

Qy       269 yGluProGlnSerGluAlaGluHisGlnArgArgAspLeuAlaArgArgLeuLysSerSe 289
Db      4788 AGAGCTGGAGGACGAGAGGAAGCAGCGCTCGATGGCAGTGGCCGCCCGGAAGAAGCTGGA 4847

Qy       289 rProArgLeuLysGluLeu---------------------------------------- 295
Db      4848 GATGGACCTGAAGGACCTGGAGGCTCACGTCGACTCGGCCAACAAGAACCGGGACGAAGC 4907

Qy       296 ----------LeuGlnAsnAlaGluValGlnSerLeuLeuSerTyrGlnArgMetArgAs 312
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Db       4908 CATCAAACAGCTGCGGAAGCTGCAGGCCCAGATGAAGGACTGCATGCGCGAGCTGGATGA 4967

Qy        312 pSerProLeuSerLysArgArgProLeuAlaMetAsnAspGluAspGluSerAlaPheAr 332

Db       4968 CACCCGCGCCTCTCGTGAGGAGATCCTGGCCCAGGCCAAAGAGAACGAGAAGAAGCTGAA 5027

Qy        332 gAlaMetGluAlaArgAlaLysLeuAspGlnLysSerGlnLeuValLeuGlyLeuHisGl 352

Db       5028 GAGCATGGAGGCC--------------GAGATGATCCAGTTGCAGGAGGAACTGGCAGC 5072

Qy        352 yPheGlyGluSerAspAspAspGluAspGluGluAspGluAsnLeuIleAspProSerGl 372

Db       5073 CGCGGAGCGTGCCAAGCGCCAGGCCCAGCAGGAGCGGGATGAGCTGGCTGACGAGATCGC 5132

Qy        372 uAsnSerPheArgArgAlaProLeuArgLeuSer-------------------------- 383

Db       5133 CAACAGCAGCGGCAAAGGAGCCCTGGCGTTAGAGGAGAAGCGGCGTCTGGAGGCCCGCAT 5192

Qy        384 -SerGlyPheValGluLysLeuLysSer------------------------AsnAspGl 395

Db       5193 CGCCCAGCTGGAGGAGGAGCTGGAGGAGGAGCAGGGCAACACGGAGCTGATCAACGACCG 5252

Qy        395 uLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAspValGluLysTyrLeuAl 415

Db       5253 GCTGAAGAAGGCC------------AACCTGCAGATCGACCAGATC-------------- 5286

Qy        415 aProLysProMetGluPheAsnProLysProGlnProGlyTyrPheAlaProArgLysIl 435

Db       5287 ------------------AACAC-CGACCTGAACCTGGA-------------------- 5306

Qy        435 eProThrArgProArgLysMetLeuProLeuLeuIleGlySerAspProLysValGlnGl 455

Db       5307 ----GCGCAGCCACGCCC-AGAAGAACGAGAATGCTCGGCAGCAGCTGGAACGCCAGAAC 5361

Qy        455 uGluIleArgArgHisProSerThrGluTrpLysIleAlaLysGluSerArgValLeuTh 475

Db       5362 AAGGAGCTTAAGGTCAAGCTGCAGGAGATGG-----------------AGGGCACTGTC 5403

Qy        475 rAsnLeuLysAsnAsnProSerLeuAlaAlaLeu---------------PheMetAspAs 490

Db       5404 AAGTCC-AAGTACAAGGCCTCCATCACCGCCCTCGAGGCCAAGATTGCACAGCTGGAGGA 5462

Qy        490 pLysLeuGluAsnThrLeuLysGlyArgGlnMetLeuThrAspGluGlnLysGlyArgTh 510

Db       5463 GCAGCTGGACAACGAGACCAAGGAGCGCCAGGCAGCCTGC---AAACAGGTGCGTCGGAC 5519

Qy        510 rArgValLys 513

Db       5520 CGAGAAGAAG 5529
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RESULT 4
US-08-533-306A-5
; Sequence 5, Application US/08533306A
; Patent No. 5837457
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; TITLE OF INVENTION: Rearrangements
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533,306A
; FILING DATE: September 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869COB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; INDIVIDUAL ISOLATE: Sample 2
; TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
; TISSUE TYPE: subtype (inv16)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 16[inv(16)(p13q22)]
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2451
US-08-533-306A-5

Alignment Scores:

Pred. No.:	3.08e-06	Length:	2680
Score:	159.00	Matches:	150
Percent Similarity:	38.3%	Conservative:	130
Best Local Similarity:	20.5%	Mismatches:	230
Query Match:	4.8%	Indels:	225
DB:	2	Gaps:	35

US-10-736-868-2 (1-643) x US-08-533-306A-5 (1-2680)

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Qy         15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaLeuLeuSer 34

Db        562 GTGGCGTCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGTTG------------------ 603

Qy         35 SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu 54

Db        604 ---CTTCAAGAAGAAACCCGGCAGAAGCTCAACGTGTCTACGAAGCTGCGCCAGCTGGAG 660

Qy         54 ------------------------------------------------------------ 54

Db        661 GAGGAGCGGAACAGCCTGCAAGACCAGCTGGACGAGGAGATGGAGGCCAAGCAGAACCTG 720

Qy         55 --------------LeuMetGlyValGlnPheValAspAlaLeuIleLysLysGlyGln 69

Db        721 GAGCGCCACATCTCCACTCTCAACATCCAGCTCTCCGACTCGAAG---AAGAAGCTGCAG 777

Qy         70 ----------------------MetGluMetAlaLysGlyAlaPheLysThrGlnLeu 81

Db        778 GACTTTGCCAGCACCGTGGAAGCTCTGGAAGAGGGGAAGAAGAGGTTCCAGAAGGAGATC 837

Qy         82 GluValLeuGluLysValHisProAspGln---------PheAspLysTyrLysLysLeu 98

Db        838 GAGAACCTCACCCAGCAGTACGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACC 897

Qy         99 Lys------------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla 112

Db        898 AAGAACAGGCTTCAGCAGGAGCTGGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA 957

Qy        113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132
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Db        958 CTCGTGTCCAACCTGGAAAAGAAGCAGAGGAAA------TTTGATCAGTTGTTAGCCGAG 1011

Qy        133 GlyIleProIleGlySerSer------------------------------------ 139

Db       1012 GAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCAGAAGCCAGG 1071

Qy        140 --------------------------IleArgGlyLeuGluAspAlaIleArgThrGln 150

Db       1072 GAGAAGGAAACCAAGGCCCTGTCCCTGGCTCGGGCCCTTGAAGAGGCCTTGGAAGCCAAA 1131

Qy        151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe 170

Db       1132 GAGGAACTCGAGCGGACCAAC---------AAAATGCTCAAAGCCGAAATGGAA------ 1176

Qy        171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189

Db       1177 ----------------------------GACCTGGTCAGCTCCAAGGATGACGTGGGC 1206

Qy        190 LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209

Db       1207 AAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGGCCCTGGAGACCCAGATGGAGGAGATG 1266

Qy        210 LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGlyGluGlu 229

Db       1267 AAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCTCG----------GAGGAC 1314

Qy        230 GlnArgMetMetMetAsnArgValAspGlnArgMetGln-----------------Gln 243

Db       1315 GCCAAACTG---------CGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCGAA 1365

Qy        244 ArgGluLeuGlnGluGluAspGluAspAspAspAspLeuGluAspGluAspValProArg 263

Db       1366 AGGGATCTCCAAGCCCGGGACGAGCAGAATGAGGAG--------------------AAG 1404

Qy        264 ArgArgSerSerAsp---------GlyGluProGlnSerGluAlaGluHisGlnArgArg 280

Db       1405 AGGAGGCAACTGCAGAGACAGCTTCACGAGTATGAGACGGAACTGGAAGACGAGCGAAAC 1464

Qy        281 AspLeuAlaArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsnAlaGlu 300

Db       1465 GAACGTGCCCTGGCAGCTGCAGCAAAGAAGAAGCTGGAAGGGGACCTGAAAGACCTGGAG 1524

Qy        301 ValGlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgPro 320

Db       1525 CTTCAGGCC---GACTCTGCCATCAAGGGGAGGGAGGAAGCCATCAAGCAGCTACGCAAA 1581

Qy        321 Leu------AlaMetAsnAsp---------------GluAspGluSerAlaPheArg--- 332

Db       1582 CTGCAGGCTCAGATGAAGGACTTTCAAAGAGAGCTGGAAGATGCCCGTGCCTCCAGAGAT 1641

Qy        333 AlaMetGluAlaArgAlaLysLeuAspGlnLysSerGlnLeuValLeuGlyLeuHisGly 352

Db       1642 GAGATCTTTGCCACAGCCAAAGAGAATGAGAAGAAAGCCAAGAGCTTG------------ 1689

Qy        353 PheGlyGluSerAspAspAspGluAspGluGluAspGluAsnLeuIleAspProSerGlu 372

Db       1690 ------GAAGCAGACCTCATGCAGCTACAAGAGGAC---------CTCGCCGCCGCTGAG 1734

Qy        373 AsnSerPheArgArgAlaProLeu---------ArgLeuSerSerGlyPheValGluLys 389

Db       1735 AGGGCTCGCAAACAAGCGGACCTCGAGAAGGAGGAACTGGCAGAGGAGCTGGCCAGTAGC 1794

Qy        390 LeuLysSerAsnAspGluLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAsp 409

Db       1795 CTGTCGGGAAGGAACGCACTCCAGGACGAGAAGCGCCGCCTGGAGGCCCGGATCGCCCAG 1854

Qy        410 ValGluLysTyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyr 429

Db       1855 CTGGAGGAGGAGCTGGAGGAGGAGCAGGG-CAACATGGAGGCCATGAGCGACCGGGTCC- 1912

Qy        430 PheAlaProArgLysIleProThr-------------------------------Arg 438

Db       1913 GCAAAGCCACACAGCAGGCCGAGCAGCTCAGCAACGAGCTGGCCACAGAGCGCAGCACGG 1972

Qy        439 ProArgLysMet---LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIle 457

Db       1973 CCCAGAAGAATGAGAGTGCCC---------GGCAGCAGCTCGAGCGGCAGAACAAGGAGC 2023

Qy        458 ArgArgHisProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeu 477

Db       2024 TCCGGAGCAAGCTCCACGAGATGGAGGGG-GCCGTCAAGTCC------------------ 2064

Qy        478 LysAsnAsnProSerLeuAlaAlaLeu---------------PheMetAspAspLysLeu 492

Db       2065 AAGTTCAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTC 2124

Qy        493 GluAsnThrLeuLysGlyArgGlnMetLeuThr-------------------------- 503

Db       2125 GAGCAGGAGGCCAGAGAGAAACAGGCAGCCACCAAGTCGCTGAAGCAGAAAGACAAGAAG 2184

Qy        504 --------------------------AspGlu--------------------------- 505

Db       2185 CTGAAGGAAATCTTGCTGCAGGTGGAGGACGAGCGCAAGATGGCCGAGCAGTACAAGGAG 2244

Qy        506 ------GlnLysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGly 523

Db       2245 CAGGCAGAGAAAGGCAATGCCAGGGTCAAGCAGCTCAAG---------AGGCAGCTGGAG 2295

Qy        524 AlaProThrAlaLysAlaGluMetIleAspAla---------LysValPheGlnAspIle 540

Db       2296 GAGGCAGAGGAGGAGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGAGCTG 2355

Qy        541 GluGluArgProIleProProLeuPhePheGluProLysGlyArgHisThrArgLeuArg 560

Db       2356 GATGAGGCC------------------------------------------------- 2364

Qy        561 TrpThrGlyAlaAsnGlu---------LysGluIleProGlyLeuGlySerArgPheIle 577

Db       2365 ---ACGGAGAGCAACGAGGCCATGGGCCGTGAGGTGAACGCACTCAAGAGCAAGCTCAGA 2421

Qy        578 LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSerThrGlnGlyArg 597

Db       2422 GGGCCCCCC--------------CCACAGGA-AACTTCGCAGTGATGCACCAGGCGAGG 2465

Qy        598 AlaArgAspGluTrpAspThrMetPheLysIle 608

Db       2466 AAACGAGACCTCTTTCGTTCCTTCTAGAAGGTC 2498
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RESULT 5
US-08-742-923A-5
; Sequence 5, Application US/08742923A
; Patent No. 5869611
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; TITLE OF INVENTION: Rearrangements
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,923A
; FILING DATE: No. 5869611ember 1, 1996
; CLASSIFICATION: 435

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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, DeAnn F.
;      REGISTRATION NUMBER:  36683
;      REFERENCE/DOCKET NUMBER:  2115-00869DVC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 641-1600
;      TELEFAX:  (810) 641-0270
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      INDIVIDUAL ISOLATE:  Sample 2
;      TISSUE TYPE:  Acute myelomonocytic leukemia, M4Eo
;      TISSUE TYPE:  subtype (inv16)
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  16[inv(16)(p13q22)]
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2451
US-08-742-923A-5

Alignment Scores:
Pred. No.:              3.08e-06      Length:          2680
Score:                  159.00        Matches:         150
Percent Similarity:     38.3%         Conservative:    130
Best Local Similarity:  20.5%         Mismatches:      230
Query Match:            4.8%          Indels:          225
DB:                     2             Gaps:            35

US-10-736-868-2 (1-643) x US-08-742-923A-5 (1-2680)

Qy         15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaLeuLeuSer 34
              :::|||   ||||||:::|||         |||   :::
Db        562 GTGGCGTCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGTTG----------------- 603

Qy         35 SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu 54
                |||      ::::::   |||||||||   ::::::      :::       ||||||
Db        604 ---CTTCAAGAAGAAACCCGGCAGAAGCTCAACGTGTCTACGAAGCTGCGCCAGCTGGAG 660

Qy         54 ------------------------------------------------------------ 54

Db        661 GAGGAGCGGAACAGCCTGCAAGACCAGCTGGACGAGGAGATGGAGGCCAAGCAGAACCTG 720

Qy         55 --------------LeuMetGlyValGlnPheValAspAlaLeuIleLysLysGlyGln 69
                           :::   :::|||      |||:::      ||||||   |||
Db        721 GAGCGCCACATCTCCACTCTCAACATCCAGCTCTCCGACTCGAAG---AAGAAGCTGCAG 777

Qy         70 ----------------------MetGluMetAlaLysGlyAlaPheLysThrGlnLeu 81
                                    :::|||      |||      |||:::   ::::::
Db        778 GACTTTGCCAGCACCGTGGAAGCTCTGGAAGAGGGGAAGAAGAGGTTCCAGAAGGAGATC 837

Qy         82 GluValLeuGluLysValHisProAspGln---------PheAspLysTyrLysLysLeu 98
              |||   |||   :::   :::   ::::::         :::||||||   :::|||
Db        838 GAGAACCTCACCCAGCAGTACGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACC 897

Qy         99 Lys-----------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla 112
              |||                :::||||||||||      |||         |||:::
Db        898 AAGAACAGGCTTCAGCAGGAGCTGGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA 957

Qy        113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132
                 ::::::   |||:::   |||                |||   |||
Db        958 CTCGTGTCCAACCTGGAAAAGAAGCAGAGGAAA------TTTGATCAGTTGTTAGCCGAG 1011

Qy        133 GlyIleProIleGlySerSer---------------------------------------- 139
                       |||  |||
Db       1012 GAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCAGAAGCCAGG 1071

Qy        140 --------------------------IleArgGlyLeuGluAspAlaIleArgThrGln 150
                                       |||   ||||||:::|||:::      :::
Db       1072 GAGAAGGAAACCAAGGCCCTGTCCCTGGCTCGGGCCCTTGAAGAGGCCTTGGAAGCCAAA 1131

Qy        151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe 170
                 ::::::|||   |||:::         ::::::   ||||||   |||:::
Db       1132 GAGGAACTCGAGCGGACCAAC---------AAAATGCTCAAAGCCGAAATGGAA------ 1176

Qy        171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189
                                          ::::::::::::   |||:::
Db       1177 ----------------------------GACCTGGTCAGCTCCAAGGATGACGTGGGC 1206

Qy        190 LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209
              |||         ::::::   |||::::::   |||      :::      ::::::
Db       1207 AAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGGCCCTGGAGACCCAGATGGAGGAGATG 1266

Qy        210 LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGlyGluGlu 229
                 |||          |||                 :::              |||:::
Db       1267 AAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCTCG-----------GAGGAC 1314

Qy        230 GlnArgMetMetMetAsnArgValAspGlnArgMetGln-----------------Gln 243
                 ::::::         |||::::::      ||||||                 :::
Db       1315 GCCAAACTG---------CGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCGAA 1365

Qy        244 ArgGluLeuGlnGluGluAspGluAspAspAspAspLeuGluAspGluAspValProArg 263
              |||:::||||||      ||||||   :::::::::                      :::
Db       1366 AGGGATCTCCAAGCCCGGGACGAGCAGAATGAGGAG--------------------AAG 1404

Qy        264 ArgArgSerSerAsp---------GlyGluProGlnSerGluAlaGluHisGlnArgArg 280
              ||||||                |||   ::::::|||   |||   :::|||
Db       1405 AGGAGGCAACTGCAGAGACAGCTTCACGAGTATGAGACGGAACTGGAAGACGAGCGAAAC 1464

Qy        281 AspLeuAlaArgArgLeuLysSerSerProArgLeuLysGluLeuGluGlnAsnAlaGlu 300
              :::   |||          :::     :::|||:::     |||::::::   |||
Db       1465 GAACGTGCCCTGGCAGCTGCAGCAAAGAAGAAGCTGGAAGGGGACCTGAAAGACCTGGAG 1524

Qy        301 ValGlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgPro 320
              :::|||:::      |||      :::   |||:::      :::   :::   |||
Db       1525 CTTCAGGCC---GACTCTGCCATCAAGGGGAGGGAGGAAGCCATCAAGCAGCTACGCAAA 1581

Qy        321 Leu------AlaMetAsnAsp--------------GluAspGluSerAlaPheArg--- 332
              |||          |||   |||            ||||||      |||   |||
Db       1582 CTGCAGGCTCAGATGAAGGACTTTCAAAGAGAGCTGGAAGATGCCCGTGCCTCCAGAGAT 1641

Qy        333 AlaMetGluAlaArgAlaLysLeuAspGlnLysSerGlnLeuValLeuGlyLeuHisGly 352
                 :::   |||   ||||||   ::::::|||          |||
Db       1642 GAGATCTTTGCCACAGCCAAAGAGAATGAGAAGAAAGCCAAGAGCTTG----------- 1689

Qy        353 PheGlyGluSerAspAspAspGluAspGluGluAspGluAsnLeuIleAspProSerGlu 372
                 |||:::|||      :::   :::||||||         :::      :::|||
Db       1690 ------GAAGCAGACCTCATGCAGCTACAAGAGGAC---------CTCGCCGCCGCTGAG 1734

Qy        373 AsnSerPheArgArgAlaProLeu---------ArgLeuSerSerGlyPheValGluLys 389
                 :::   ::::::|||   |||          |||:::
Db       1735 AGGGCTCGCAAACAAGCGGACCTCGAGAAGGAGGAACTGGCAGAGGAGCTGGCCAGTAGC 1794

Qy        390 LeuLysSerAsnAspGluLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAsp 409
              |||         :::   |||:::            |||::::::   |||:::
Db       1795 CTGTCGGGAAGGAACGCACTCCAGGACGAGAAGCGCCGCCTGGAGGCCCGGATCGCCCAG 1854

Qy        410 ValGluLysTyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyr 429
              :::|||:::   |||      :::      :::                :::||||||
Db       1855 CTGGAGGAGGAGCTGGAGGAGGAGCAGGG-CAACATGGAGGCCATGAGCGACCGGGTCC- 1912

Qy        430 PheAlaProArgLysIleProThr--------------------------------Arg 438
                 |||          |||:::                                  |||
Db       1913 GCAAAGCCACACAGCAGGCCGAGCAGCTCAGCAACGAGCTGGCCACAGAGCGCAGCACGG 1972

Qy        439 ProArgLysMet---LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIle 457
              ||||||:::|||   :::|||         ||||||            :::
Db       1973 CCCAGAAGAATGAGAGTGCCC---------GGCAGCAGCTCGAGCGGCAGAACAAGGAGC 2023
```

```
Qy        458 ArgArgHisProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeu 477
                          ||||||   |||:::   |||   :::|||
Db       2024 TCCGGAGCAAGCTCCACGAGATGGAGGGG-GCCGTCAAGTCC----------------- 2064

Qy        478 LysAsnAsnProSerLeuAlaAlaLeu--------------PheMetAspAspLysLeu 492
               |||         ::::::|||||||||             ::::::::::::::
Db       2065 AAGTTCAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTC 2124

Qy        493 GluAsnThrLeuLysGlyArgGlnMetLeuThr-------------------------- 503
               |||         :::   :::|||      |||
Db       2125 GAGCAGGAGGCCAGAGAGAAACAGGCAGCCACCAAGTCGCTGAAGCAGAAAGACAAGAAG 2184

Qy        504 --------------------------AspGlu--------------------------- 505
                                         ||||||
Db       2185 CTGAAGGAAATCTTGCTGCAGGTGGAGGACGAGCGCAAGATGGCCGAGCAGTACAAGGAG 2244

Qy        506 ------GlnLysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGly 523
                  :::||||||      |||||||||   ::::::         |||
Db       2245 CAGGCAGAGAAAGGCAATGCCAGGGTCAAGCAGCTCAAG---------AGGCAGCTGGAG 2295

Qy        524 AlaProThrAlaLysAlaGluMetIleAspAla---------LysValPheGlnAspIle 540
                          :::::::::   |||:::|||         |||:::   :::::::::
Db       2296 GAGGCAGAGGAGGAGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGAGCTG 2355

Qy        541 GluGluArgProIleProProLeuPhePheGluProLysGlyArgHisThrArgLeuArg 560
               :::|||
Db       2356 GATGAGGCC-------------------------------------------------- 2364

Qy        561 TrpThrGlyAlaAsnGlu---------LysGluIleProGlyLeuGlySerArgPheIle 577
                  |||   :::||||||         :::|||:::      |||   |||:::
Db       2365 ---ACGGAGAGCAACGAGGCCATGGGCCGTGAGGTGAACGCACTCAAGAGCAAGCTCAGA 2421

Qy        578 LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSerThrGlnGlyArg 597
                  |||                |||      |||   |||         |||   |||
Db       2422 GGGCCCCCC--------------CCACAGGA-AACTTCGCAGTGATGCACCAGGCGAGG 2465

Qy        598 AlaArgAspGluTrpAspThrMetPheLysIle 608
                  ||||||   :::   :::     |||:::
Db       2466 AAACGAGACCTCTTTCGTTCCTTCTAGAAGGTC 2498

RESULT 6
US-08-533-306A-3
; Sequence 3, Application US/08533306A
; Patent No. 5837457
;  GENERAL INFORMATION:
;    APPLICANT:  Liu, Pu
;    APPLICANT:  Collins, Francis S.
;    APPLICANT:  Siciliano, Michael J.
;    APPLICANT:  Claxton, David
;    TITLE OF INVENTION:  Markers for Detection of Chromosome 16
;    TITLE OF INVENTION:  Rearrangements
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Harness, Dickey & Pierce, P.L.C.
;      STREET:  P.O. Box 828
;      CITY:  Bloomfield Hills
;      STATE:  MI
;      COUNTRY:  USA
;      ZIP:  48303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/533,306A
;      FILING DATE:  September 25, 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, DeAnn F.
;      REGISTRATION NUMBER:  36683
;      REFERENCE/DOCKET NUMBER:  2115-00869COB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 641-1600
;      TELEFAX:  (810) 641-0270
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2887 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      INDIVIDUAL ISOLATE:  Sample 1
;      TISSUE TYPE:  Acute myelomonocytic leukemia, M4Eo
;      TISSUE TYPE:  subtype (inv16)
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  16[inv(16)(p13q22)]
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2658
US-08-533-306A-3

Alignment Scores:
Pred. No.:              3.46e-06        Length:         2887
Score:                  159.00          Matches:        150
Percent Similarity:     38.3%           Conservative:   130
Best Local Similarity:  20.5%           Mismatches:     230
Query Match:            4.8%            Indels:         225
DB:                     2               Gaps:           35

US-10-736-868-2 (1-643) x US-08-533-306A-3 (1-2887)

Qy         15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaLeuLeuSer 34
                 :::|||   ||||||:::|||          |||   :::
Db        769 GTGGCGTCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGTTG----------------- 810

Qy         35 SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu 54
                  |||      ::::::   |||||||||  ::::::      :::      ||||||
Db        811 ---CTTCAAGAAGAAACCCGGCAGAAGCTCAACGTGTCTACGAAGCTGCGCCAGCTGGAG 867

Qy         54 ------------------------------------------------------------ 54

Db        868 GAGGAGCGGAACAGCCTGCAAGACCAGCTGGACGAGGAGATGGAGGCCAAGCAGAACCTG 927

Qy         55 --------------LeuMetGlyValGlnPheValAspAlaLeuIleLysLysGlyGln 69
                             :::   :::|||      |||:::      ||||||   |||
Db        928 GAGCGCCACATCTCCACTCTCAACATCCAGCTCTCCGACTCGAAG---AAGAAGCTGCAG 984

Qy         70 ----------------------MetGluMetAlaLysGlyAlaPheLysThrGlnLeu 81
                                    :::|||      |||      |||:::   ::::::
Db        985 GACTTTGCCAGCACCGTGGAAGCTCTGGAAGAGGGGAAGAAGAGGTTCCAGAAGGAGATC 1044

Qy         82 GluValLeuGluLysValHisProAspGln---------PheAspLysTyrLysLysLeu 98
                 |||   |||   :::   :::   ::::::         :::||||||   :::|||
Db       1045 GAGAACCTCACCCAGCAGTACGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACC 1104

Qy         99 Lys------------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla 112
                 |||                 :::|||||||||      |||         |||:::
Db       1105 AAGAACAGGCTTCAGCAGGAGCTGGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA 1164

Qy        113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132
                  ::::::   |||:::   |||                |||   |||
Db       1165 CTCGTGTCCAACCTGGAAAAGAAGCAGAGGAAA------TTTGATCAGTTGTTAGCCGAG 1218

Qy        133 GlyIleProIleGlySerSer---------------------------------------- 139
                       |||   |||
Db       1219 GAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCAGAAGCCAGG 1278

Qy        140 --------------------------IleArgGlyLeuGluAspAlaIleArgThrGln 150
                                         |||   ||||||:::|||:::      :::
Db       1279 GAGAAGGAAACCAAGGCCCTGTCCCTGGCTCGGGCCCTTGAAGAGGCCTTGGAAGCCAAA 1338
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Qy       151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe 170
Db      1339 GAGGAACTCGAGCGGACCAAC---------AAAATGCTCAAAGCCGAAATGGAA------ 1383

Qy       171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189
Db      1384 ----------------------------GACCTGGTCAGCTCCAAGGATGACGTGGGC 1413

Qy       190 LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209
Db      1414 AAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGGCCCTGGAGACCCAGATGGAGGAGATG 1473

Qy       210 LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGlyGluGlu 229
Db      1474 AAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCTCG----------GAGGAC 1521

Qy       230 GlnArgMetMetMetAsnArgValAspGlnArgMetGln----------------Gln 243
Db      1522 GCCAAACTG---------CGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCGAA 1572

Qy       244 ArgGluLeuGlnGluGluAspGluAspAspAspAspLeuGluAspGluAspValProArg 263
Db      1573 AGGGATCTCCAAGCCCGGGACGAGCAGAATGAGGAG----------------AAG 1611

Qy       264 ArgArgSerSerAsp---------GlyGluProGlnSerGluAlaGluHisGlnArgArg 280
Db      1612 AGGAGGCAACTGCAGAGACAGCTTCACGAGTATGAGACGGAACTGGAAGACGAGCGAAAC 1671

Qy       281 AspLeuAlaArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsnAlaGlu 300
Db      1672 GAACGTGCCCTGGCAGCTGCAGCAAAGAAGAAGCTGGAAGGGGACCTGAAAGACCTGGAG 1731

Qy       301 ValGlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgPro 320
Db      1732 CTTCAGGCC---GACTCTGCCATCAAGGGGAGGGAGGAAGCCATCAAGCAGCTACGCAAA 1788

Qy       321 Leu------AlaMetAsnAsp----------------GluAspGluSerAlaPheArg--- 332
Db      1789 CTGCAGGCTCAGATGAAGGACTTTCAAAGAGAGCTGGAAGATGCCCGTGCCTCCAGAGAT 1848

Qy       333 AlaMetGluAlaArgAlaLysLeuAspGlnLysSerGlnLeuValLeuGlyLeuHisGly 352
Db      1849 GAGATCTTTGCCACAGCCAAAGAGAATGAGAAGAAAGCCAAGAGCTTG------------ 1896

Qy       353 PheGlyGluSerAspAspAspGluAspGluGluAspGluAsnLeuIleAspProSerGlu 372
Db      1897 ------GAAGCAGACCTCATGCAGCTACAAGAGGAC---------CTCGCCGCCGCTGAG 1941

Qy       373 AsnSerPheArgArgAlaProLeu---------ArgLeuSerSerGlyPheValGluLys 389
Db      1942 AGGGCTCGCAAACAAGCGGACCTCGAGAAGGAGGAACTGGCAGAGGAGCTGGCCAGTAGC 2001

Qy       390 LeuLysSerAsnAspGluLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAsp 409
Db      2002 CTGTCGGGAAGGAACGCACTCCAGGACGAGAAGCGCCGCCTGGAGGCCCGGATCGCCCAG 2061

Qy       410 ValGluLysTyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyr 429
Db      2062 CTGGAGGAGGAGCTGGAGGAGGAGCAGGG-CAACATGGAGGCCATGAGCGACCGGGTCC- 2119

Qy       430 PheAlaProArgLysIleProThr----------------------------------Arg 438
Db      2120 GCAAAGCCACACAGCAGGCCGAGCAGCTCAGCAACGAGCTGGCCACAGAGCGCAGCACGG 2179

Qy       439 ProArgLysMet---LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIle 457
Db      2180 CCCAGAAGAATGAGAGTGCCC---------GGCAGCAGCTCGAGCGGCAGAACAAGGAGC 2230

Qy       458 ArgArgHisProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeu 477
Db      2231 TCCGGAGCAAGCTCCACGAGATGGAGGGG-GCCGTCAAGTCC------------------ 2271

Qy       478 LysAsnAsnProSerLeuAlaAlaLeu----------------PheMetAspAspLysLeu 492

Db      2272 AAGTTCAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTC 2331

Qy       493 GluAsnThrLeuLysGlyArgGlnMetLeuThr---------------------------- 503
Db      2332 GAGCAGGAGGCCAGAGAGAAACAGGCAGCCACCAAGTCGCTGAAGCAGAAAGACAAGAAG 2391

Qy       504 ----------------------------AspGlu---------------------------- 505
Db      2392 CTGAAGGAAATCTTGCTGCAGGTGGAGGACGAGCGCAAGATGGCCGAGCAGTACAAGGAG 2451

Qy       506 ------GlnLysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGly 523
Db      2452 CAGGCAGAGAAAGGCAATGCCAGGGTCAAGCAGCTCAAG---------AGGCAGCTGGAG 2502

Qy       524 AlaProThrAlaLysAlaGluMetIleAspAla---------LysValPheGlnAspIle 540
Db      2503 GAGGCAGAGGAGGAGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGAGCTG 2562

Qy       541 GluGluArgProIleProProLeuPhePheGluProLysGlyArgHisThrArgLeuArg 560
Db      2563 GATGAGGCC---------------------------------------------------- 2571

Qy       561 TrpThrGlyAlaAsnGlu---------LysGluIleProGlyLeuGlySerArgPheIle 577
Db      2572 ---ACGGAGAGCAACGAGGCCATGGGCCGTGAGGTGAACGCACTCAAGAGCAAGCTCAGA 2628

Qy       578 LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSerThrGlnGlyArg 597
Db      2629 GGGCCCCCC--------------CCACAGGA-AACTTCGCAGTGATGCACCAGGCGAGG 2672

Qy       598 AlaArgAspGluTrpAspThrMetPheLysIle 608
Db      2673 AAACGAGACCTCTTTCGTTCCTTCTAGAAGGTC 2705
```

RESULT 7
US-08-742-923A-3
; Sequence 3, Application US/08742923A
; Patent No. 5869611
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; TITLE OF INVENTION: Rearrangements
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,923A
; FILING DATE: No. 5869611ember 1, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869DVC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2887 base pairs

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;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       INDIVIDUAL ISOLATE:  Sample 1
;       TISSUE TYPE:  Acute myelomonocytic leukemia, M4Eo
;       TISSUE TYPE:  subtype (inv16)
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:  16[inv(16)(p13q22)]
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..2658
US-08-742-923A-3

Alignment Scores:
Pred. No.:              3.46e-06        Length:         2887
Score:                  159.00          Matches:        150
Percent Similarity:     38.3%           Conservative:   130
Best Local Similarity:  20.5%           Mismatches:     230
Query Match:            4.8%            Indels:         225
DB:                     2               Gaps:           35

US-10-736-868-2 (1-643) x US-08-742-923A-3 (1-2887)

Qy         15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaLeuLeuSer 34
              :::|||   ||||||:::|||         |||   :::
Db        769 GTGGCGTCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGTTG------------------ 810

Qy         35 SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu 54
                 |||      ::::::   |||||||||   ::::::      :::      ||||||
Db        811 ---CTTCAAGAAGAAACCCGGCAGAAGCTCAACGTGTCTACGAAGCTGCGCCAGCTGGAG 867

Qy         54 ------------------------------------------------------------ 54

Db        868 GAGGAGCGGAACAGCCTGCAAGACCAGCTGGACGAGGAGATGGAGGCCAAGCAGAACCTG 927

Qy         55 ---------------LeuMetGlyValGlnPheValAspAlaLeuIleLysLysGlyGln 69
                           :::   :::|||      |||:::      ||||||   |||
Db        928 GAGCGCCACATCTCCACTCTCAACATCCAGCTCTCCGACTCGAAG---AAGAAGCTGCAG 984

Qy         70 ------------------------MetGluMetAlaLysGlyAlaPheLysThrGlnLeu 81
                                  :::|||      |||      |||:::   ::::::
Db        985 GACTTTGCCAGCACCGTGGAAGCTCTGGAAGAGGGGAAGAAGAGGTTCCAGAAGGAGATC 1044

Qy         82 GluValLeuGluLysValHisProAspGln---------PheAspLysTyrLysLysLeu 98
              |||   |||   :::   :::   ::::::         :::||||||   :::|||
Db       1045 GAGAACCTCACCCAGCAGTACGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACC 1104

Qy         99 Lys------------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla 112
              |||                  :::||||||||      |||         |||:::
Db       1105 AAGAACAGGCTTCAGCAGGAGCTGGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA 1164

Qy        113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132
                 ::::::   |||:::   |||                  |||   |||
Db       1165 CTCGTGTCCAACCTGGAAAAGAAGCAGAGGAAA------TTTGATCAGTTGTTAGCCGAG 1218

Qy        133 GlyIleProIleGlySerSer---------------------------------------- 139
                       |||  |||
Db       1219 GAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCAGAAGCCAGG 1278

Qy        140 --------------------------IleArgGlyLeuGluAspAlaIleArgThrGln 150
                                       |||   ||||||:::|||:::      :::
Db       1279 GAGAAGGAAACCAAGGCCCTGTCCCTGGCTCGGGCCCTTGAAGAGGCCTTGGAAGCCAAA 1338

Qy        151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe 170
                 ::::::|||   |||:::         ::::::   ||||||   |||:::
Db       1339 GAGGAACTCGAGCGGACCAAC---------AAAATGCTCAAAGCCGAAATGGAA------ 1383

Qy        171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189

Db       1384 ----------------------------GACCTGGTCAGCTCCAAGGATGACGTGGGC 1413

Qy        190 LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209
              |||         ::::::   |||::::::   |||      :::      ::::::
Db       1414 AAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGGCCCTGGAGACCCAGATGGAGGAGATG 1473

Qy        210 LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGlyGluGlu 229
                 |||         |||                 :::          |||:::
Db       1474 AAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCTCG-----------GAGGAC 1521

Qy        230 GlnArgMetMetMetAsnArgValAspGlnArgMetGln-----------------Gln 243
                 ::::::         |||:::::      ||||||                 :::
Db       1522 GCCAAACTG---------CGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCGAA 1572

Qy        244 ArgGluLeuGlnGluGluAspGluAspAspAspAspLeuGluAspGluAspValProArg 263
              |||:::||||||      ||||||  :::::::::                     :::
Db       1573 AGGGATCTCCAAGCCCGGGACGAGCAGAATGAGGAG--------------------AAG 1611

Qy        264 ArgArgSerSerAsp---------GlyGluProGlnSerGluAlaGluHisGlnArgArg 280
              ||||||                  |||  ::::::|||   |||   :::|||
Db       1612 AGGAGGCAACTGCAGAGACAGCTTCACGAGTATGAGACGGAACTGGAAGACGAGCGAAAC 1671

Qy        281 AspLeuAlaArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsnAlaGlu 300
                 :::   |||            :::      :::|||:::      |||::::::   |||
Db       1672 GAACGTGCCCTGGCAGCTGCAGCAAAGAAGAAGCTGGAAGGGGACCTGAAAGACCTGGAG 1731

Qy        301 ValGlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgPro 320
              :::|||:::      |||      :::   |||:::      :::   :::   |||
Db       1732 CTTCAGGCC---GACTCTGCCATCAAGGGGAGGGAGGAAGCCATCAAGCAGCTACGCAAA 1788

Qy        321 Leu------AlaMetAsnAsp--------------GluAspGluSerAlaPheArg--- 332
              |||          |||  |||             ||||||      |||   |||
Db       1789 CTGCAGGCTCAGATGAAGGACTTTCAAAGAGAGCTGGAAGATGCCCGTGCCTCCAGAGAT 1848

Qy        333 AlaMetGluAlaArgAlaLysLeuAspGlnLysSerGlnLeuValLeuGlyLeuHisGly 352
                 :::   |||   ||||||   ::::::|||            |||
Db       1849 GAGATCTTTGCCACAGCCAAAGAGAATGAGAAGAAAGCCAAGAGCTTG------------ 1896

Qy        353 PheGlyGluSerAspAspAspGluAspGluGluAspGluAsnLeuIleAspProSerGlu 372
                 |||:::|||      :::   :::||||||          :::      :::|||
Db       1897 ------GAAGCAGACCTCATGCAGCTACAAGAGGAC---------CTCGCCGCCGCTGAG 1941

Qy        373 AsnSerPheArgArgAlaProLeu---------ArgLeuSerSerGlyPheValGluLys 389
                 :::   ::::::|||   |||            |||:::
Db       1942 AGGGCTCGCAAACAAGCGGACCTCGAGAAGGAGGAACTGGCAGAGGAGCTGGCCAGTAGC 2001

Qy        390 LeuLysSerAsnAspGluLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAsp 409
              |||         :::   |||:::            |||::::::   |||:::
Db       2002 CTGTCGGGAAGGAACGCACTCCAGGACGAGAAGCGCCGCCTGGAGGCCCGGATCGCCCAG 2061

Qy        410 ValGluLysTyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyr 429
              :::|||:::   |||      :::      :::              :::||||||
Db       2062 CTGGAGGAGGAGCTGGAGGAGGAGCAGGG-CAACATGGAGGCCATGAGCGACCGGGTCC- 2119

Qy        430 PheAlaProArgLysIleProThr---------------------------------Arg 438
                 |||      |||:::                                    |||
Db       2120 GCAAAGCCACACAGCAGGCCGAGCAGCTCAGCAACGAGCTGGCCACAGAGCGCAGCACGG 2179

Qy        439 ProArgLysMet---LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIle 457
              ||||||:::|||   :::|||         ||||||             :::
Db       2180 CCCAGAAGAATGAGAGTGCCC---------GGCAGCAGCTCGAGCGGCAGAACAAGGAGC 2230

Qy        458 ArgArgHisProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeu 477
                       ||||||   |||:::   |||   :::|||
Db       2231 TCCGGAGCAAGCTCCACGAGATGGAGGGG-GCCGTCAAGTCC----------------- 2271

Qy        478 LysAsnAsnProSerLeuAlaAlaLeu---------------PheMetAspAspLysLeu 492
              |||         ::::::||||||||||              ::::::::::::::
Db       2272 AAGTTCAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTC 2331

Qy        493 GluAsnThrLeuLysGlyArgGlnMetLeuThr-------------------------- 503
              |||         :::   :::|||      |||
```

```
Db       2332 GAGCAGGAGGCCAGAGAGAAACAGGCAGCCACCAAGTCGCTGAAGCAGAAAGACAAGAAG 2391

Qy        504 --------------------------AspGlu-------------------------- 505

Db       2392 CTGAAGGAAATCTTGCTGCAGGTGGAGGACGAGCGCAAGATGGCCGAGCAGTACAAGGAG 2451

Qy        506 ------GlnLysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGly 523

Db       2452 CAGGCAGAGAAAGGCAATGCCAGGGTCAAGCAGCTCAAG---------AGGCAGCTGGAG 2502

Qy        524 AlaProThrAlaLysAlaGluMetIleAspAla---------LysValPheGlnAspIle 540

Db       2503 GAGGCAGAGGAGGAGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGAGCTG 2562

Qy        541 GluGluArgProIleProProLeuPhePheGluProLysGlyArgHisThrArgLeuArg 560

Db       2563 GATGAGGCC---------------------------------------------------- 2571

Qy        561 TrpThrGlyAlaAsnGlu---------LysGluIleProGlyLeuGlySerArgPheIle 577

Db       2572 ---ACGGAGAGCAACGAGGCCATGGGCCGTGAGGTGAACGCACTCAAGAGCAAGCTCAGA 2628

Qy        578 LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSerThrGlnGlyArg 597

Db       2629 GGGCCCCCC---------------CCACAGGA-AACTTCGCAGTGATGCACCAGGCGAGG 2672

Qy        598 AlaArgAspGluTrpAspThrMetPheLysIle 608

Db       2673 AAACGAGACCTCTTTCGTTCCTTCTAGAAGGTC 2705
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RESULT 8
US-09-949-016-1019
; Sequence 1019, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1019
; LENGTH: 4935
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1019

Alignment Scores:

Pred. No.:	8.04e-06	Length:	4935
Score:	159.00	Matches:	159
Percent Similarity:	36.1%	Conservative:	97
Best Local Similarity:	22.4%	Mismatches:	260
Query Match:	4.8%	Indels:	196
DB:	3	Gaps:	35

US-10-736-868-2 (1-643) x US-09-949-016-1019 (1-4935)

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Qy         23 ProSerThrSerAspAlaProGlyAlaLeuLeuSer---SerLeuValGlyLysSerHis 41

Db        484 CCGAGTACCTCACGCAAGATGGCGGAGCTGGAGGAGGTGACTCTGGACGGGAAGCCTCTT 543

Qy         42 GlnLysLeuProLeuAlaProSerMetGluAlaLeuGluLeuMetGlyValGlnPheVal 61

Db        544 CAGGCGCTGCGGGTGACCGACCTGAAGGCCGCACTGGAGCAGCGAGGC------------ 591

Qy         62 AspAlaLeuIleLysLysGlyGln-----------MetGluMetAlaLysGly------ 75

Db        592 ------CTAGCCAAGAGCGGGCAGAAGAGTGCCCTGGTCAAGCGGCTCAAAGGGGCTCTA 645

Qy         76 ------------------------------------AlaPheLysThrGlnLeuGlu 82

Db        646 ATGCTAGAAAATTTACAGAAACACTCAACACCCCATGCTGCATTCCAGCCAAATTCCCAG 705

Qy         83 ValLeuGluLysValHisProAspGlnPheAspLysTyrLysLysLeuLysValAspAsp 102

Db        706 ATTGGTGAGGAAATGAGCCAGAACAGTTTCATAAAACAGTATCTGGAAAAGCAGCAGGAG 765

Qy        103 LeuAlaAlaAspAlaValMetGlnGlnAla---GluMetAlaLysLeuGlnProLysSer 121

Db        766 CTACTTAGGCAGCGTCTGGAACGTGAAGCTCGAGAAGCTGCAGAACTTGAAGAAGCTTCA 825

Qy        122 GlyAsnAlaPheIleAspMetLeuAsnGlyAsnGlyIle-----------------Pro 135

Db        826 GCTGAGTCGGAGGACGAGATGATCCATCCTGAGGGAGTGGCTTCCCTGCTGCCTCCTGAC 885

Qy        136 IleGlySerSerIleArgGlyLeuGluAspAlaIleArgThrGlnArgAspMetGluAsn 155

Db        886 TTTCAGAGCAGCCTGGAGAGACCAGAGCTGGAGCTCAGCAGACATTCGCCCAGAAAAAGC 945

Qy        156 ThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPheGlnThrGlnIleLeu 175

Db        946 TCCTCAATTTCTGAAGAG---------------------------------------- 963

Qy        176 ProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPheLysMetProGlnGlnMet 195

Db        964 ----------------------AAAGGTGACTCTGATGATGAGAAACCA--------- 990

Qy        196 ArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAlaLeuAlaGlnArgAlaMet 215

Db        991 AGGAAAGGAGAAAGACGATCATCTAGGGTC---AGACAGGCAAGAGCAGCTAAACTGTCT 1047

Qy        216 LeuGlyLysAsnAlaProValAlaGlyGlyArgGly-GluGlu------GlnArgMetMe 233

Db       1048 GAGGGC---AGCCAACCTGCTGA-GGAGGAAGAGGATCAAGAAACACCTTCCAGAAACCT 1103

Qy        233 tMetAsnArgValAspGlnArgMet------GlnGlnArgGluLeuGlnGluGluAspGl 251

Db       1104 AAGGGTCAGAGCAGATCGAAATTTGAAAACAGAGGAGGAAGAAGAGGAGGAGGAGGAGGA 1163

Qy        251 uAspAspAspAspLeuGluAspGluAspValProArgArgArgSerSerAspGlyGluPr 271

Db       1164 GGAAGAAGATGATGAAGAAGAGGAA--------------------GGTGATGATGAGGG 1202

Qy        271 oGlnSerGluAlaGluHisGlnArgArgAspLeuAlaArgArgLeuLysSerSerProAr 291

Db       1203 ACAAAAATCTAGGGAG---------------------------------GCACCAAT 1226

Qy        291 gLeuLysGluLeuLeuGlnAsnAlaGluValGlnSerLeuLeuSerTyrGlnArgMetAr 311

Db       1227 CCTGAAAGAGTTTAAGGAAGAAGGGGAA--------------GAGATACCTAGAGTAAA 1271

Qy        311 gAspSerProLeuSerLysArgArgProLeuAlaMetAsnAspGluAspGlu-------- 328

Db       1272 ACCAGAGGAGATGATGGATGAGAGACCCAAAACAAGATCCCAGGAACAGGAGGTGTTAGA 1331

Qy        329 -------SerAlaPheArgAlaMetGluAlaArgAlaLysLeuAspGlnLysSerGlnLe 346

Db       1332 GAGAGGAGGGAGATTTACAAGATCCCAGGAAGAGGCTAGA---------AAAAGTCATCT 1382

Qy        346 uValLeuGlyLeuHisGlyPheGlyGluSerAspAspAspGluAspGluGluAspGluAs 366

Db       1383 GGCC-----------------------------AGACAGCAGCAGGAGAAGGAAATGAA 1412

Qy        366 nLeuIleAspProSerGluAsnSerPheArgArgAlaProLeuArgLeuSerSerGlyPh 386

Db       1413 AACAACATCTCCCCTTGAGGAGGAAGAAAGAGAA------ATAAAATCTTCACAAGGCTT 1466

Qy        386 eValGluLysLeuLysSer--------------------AsnAspGluLeuLysSerAl 399
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Db       1467 AAAGGAAAAATCGAAGTCTCCTTCCCCTCCTCGACTGACTGAAGATCGAAAGAAGGCCTC 1526

Qy        399 aLeuAspArgIleLysTyrArgValAspAspValGluLysTyrLeuAlaProLysProMe 419

Db       1527 ACTTGTAGCGCTGCCAGAGCAAACTGCCAGCGAGGAGGAG------ACTCCTCCACCTTT 1580

Qy        419 t------------GluPheAsnProLysProGlnProGlyTyrPheAlaProArgLysIl 435

Db       1581 ACTAACAAAGGAAGCATCTTCTCCACCACCTCATCCACAGCTCCATAGCGAAGAAGAAAT 1640

Qy        435 e---------------ProThrArgPro------------------------------- 439

Db       1641 AGAGCCCATGGAAGGCCCAGCCCCCCCTGTCCTCATTCAGTTATCTCCTCCTAATACAGA 1700

Qy        440 ----------ArgLysMetLeu---------------------------------------- 443

Db       1701 TGCTGACACCAGGGAGCTATTAGTATCTCAGCATACTGTCCAGTTGGTAGGAGGCCTGTC 1760

Qy        444 -ProLeuLeuIleGlySerAsp-ProLys---------ValGlnGluGluIleArgArgH 460

Db       1761 TCCTTTGTCAAGTCCTTCAGACACCAAAGCAGAATCTCCAGCAGAGAAAGTGCCAGAGGA 1820

Qy        460 isProSerThrGluTrp---------------LysIleAlaLysGluSerArgValLeuT 475

Db       1821 GAGTGTCCTGCCTCTGGTTCAGAAAAGCACACTGGCTGACTACTCAGCCCAGAAGGATCT 1880

Qy        475 hrAsnLeuLysAsn------------AsnProSerLeuAlaAlaLeu------------P 487

Db       1881 TGAACCTGAGTCAGACAGATCTGCTCAGCCCCTCCCTCTAAAAATTGAGGAATTAGCACT 1940

Qy        487 heMetAspAspLysLeuGluAsnThrLeuLysGlyArgGlnMetLeuThrAspGluGlnL 507

Db       1941 GGCCAAAGGAATCACTGAAGAATGT-CTGAAA------CAGCCATCTTTGGAACAGAAGG 1993

Qy        507 ysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGlyAlaProThrA 527

Db       1994 AAGGCAGAAGAGCTTCTCATACCCTTCTCCCAAGCCACAGATTGAAACAGTCAGCTGATT 2053

Qy        527 laLysAlaGluMetIleAspAlaLysValPheGlnAspIleGluGluArgProIleProP 547

Db       2054 CATCCTCTAGCCGGTCCTCCTCATCTTCCTCCTCCAGTTCTAGATCAAGATCTCGCTCTC 2113

Qy        547 roLeuPhePheGluProLysGly------ArgHisThrArgLeuArg------------ 560

Db       2114 CT---------GACAGTTCAGGTTCTCGGTCTCATTCACCGCTCAGATCCAAGCAGAGAG 2164

Qy        561 -------------TrpThrGlyAlaAsnGluLysGluIleProGlyLeuGlySerArgP 576

Db       2165 ATGTAGCCCAGGCACGTACTCATGCCAACCCTCGTGGTAGACCCAAGATGGGCTCCAGAT 2224

Qy        576 heIleLeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSer------- 593

Db       2225 CAACATCAGAGTCCAGATCAAGGTCACGTTCACGTTCTCGTTCAGCATCAAGCAACAGCA 2284

Qy        594 -----------ThrGlnGlyArgAlaArgAspGluTrpAspThrMetPheLysIleProA 610

Db       2285 GAAAATCTCTGAGCCCTGGAGTCTCCAGGGACAGC---AGCACCAGCTATACTGAAACCA 2341

Qy        610 snAsnTrpAsnProGlyAspGluVal 618

Db       2342 AAGATCCCTCTTCTGGTCAGGAGGTT 2367

RESULT 9
US-09-949-016-5054
; Sequence 5054, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5054
;   LENGTH: 4935
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5054

Alignment Scores:
Pred. No.:                8.04e-06      Length:          4935
Score:                    159.00        Matches:         159
Percent Similarity:       36.1%         Conservative:    97
Best Local Similarity:    22.4%         Mismatches:      260
Query Match:              4.8%          Indels:          196
DB:                       3             Gaps:            35

US-10-736-868-2 (1-643) x US-09-949-016-5054 (1-4935)

Qy         23 ProSerThrSerAspAlaProGlyAlaLeuLeuSer---SerLeuValGlyLysSerHis 41

Db        485 CCGAGTACCTCACGCAAGATGGCGGAGCTGGAGGAGGTGACTCTGGACGGGAAGCCTCTT 544

Qy         42 GlnLysLeuProLeuAlaProSerMetGluAlaLeuGluLeuMetGlyValGlnPheVal 61

Db        545 CAGGCGCTGCGGGTGACCGACCTGAAGGCCGCACTGGAGCAGCGAGGC------------ 592

Qy         62 AspAlaLeuIleLysLysGlyGln------------MetGluMetAlaLysGly------ 75

Db        593 ------CTAGCCAAGAGCGGGCAGAAGAGTGCCCTGGTCAAGCGGCTCAAAGGGGCTCTA 646

Qy         76 ------------------------------------AlaPheLysThrGlnLeuGlu 82

Db        647 ATGCTAGAAAATTTACAGAAACACTCAACACCCCATGCTGCATTCCAGCCAAATTCCCAG 706

Qy         83 ValLeuGluLysValHisProAspGlnPheAspLysTyrLysLysLeuLysValAspAsp 102

Db        707 ATTGGTGAGGAAATGAGCCAGAACAGTTTCATAAAACAGTATCTGGAAAAGCAGCAGGAG 766

Qy        103 LeuAlaAlaAspAlaValMetGlnGlnAla---GluMetAlaLysLeuGlnProLysSer 121

Db        767 CTACTTAGGCAGCGTCTGGAACGTGAAGCTCGAGAAGCTGCAGAACTTGAAGAAGCTTCA 826

Qy        122 GlyAsnAlaPheIleAspMetLeuAsnGlyAsnGlyIle------------------Pro 135

Db        827 GCTGAGTCGGAGGACGAGATGATCCATCCTGAGGGAGTGGCTTCCCTGCTGCCTCCTGAC 886

Qy        136 IleGlySerSerIleArgGlyLeuGluAspAlaIleArgThrGlnArgAspMetGluAsn 155

Db        887 TTTCAGAGCAGCCTGGAGAGACCAGAGCTGGAGCTCAGCAGACATTCGCCCAGAAAAAGC 946

Qy        156 ThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPheGlnThrGlnIleLeu 175

Db        947 TCCTCAATTTCTGAAGAG---------------------------------------- 964

Qy        176 ProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPheLysMetProGlnGlnMet 195

Db        965 ----------------------AAAGGTGACTCTGATGATGAGAAACCA--------- 991

Qy        196 ArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAlaLeuAlaGlnArgAlaMet 215

Db        992 AGGAAAGGAGAAAGACGATCATCTAGGGTC---AGACAGGCAAGAGCAGCTAAACTGTCT 1048

Qy        216 LeuGlyLysAsnAlaProValAlaGlyGlyArgGly-GluGlu------GlnArgMetMe 233

Db       1049 GAGGGC---AGCCAACCTGCTGA-GGAGGAAGAGGATCAAGAAACACCTTCCAGAAACCT 1104
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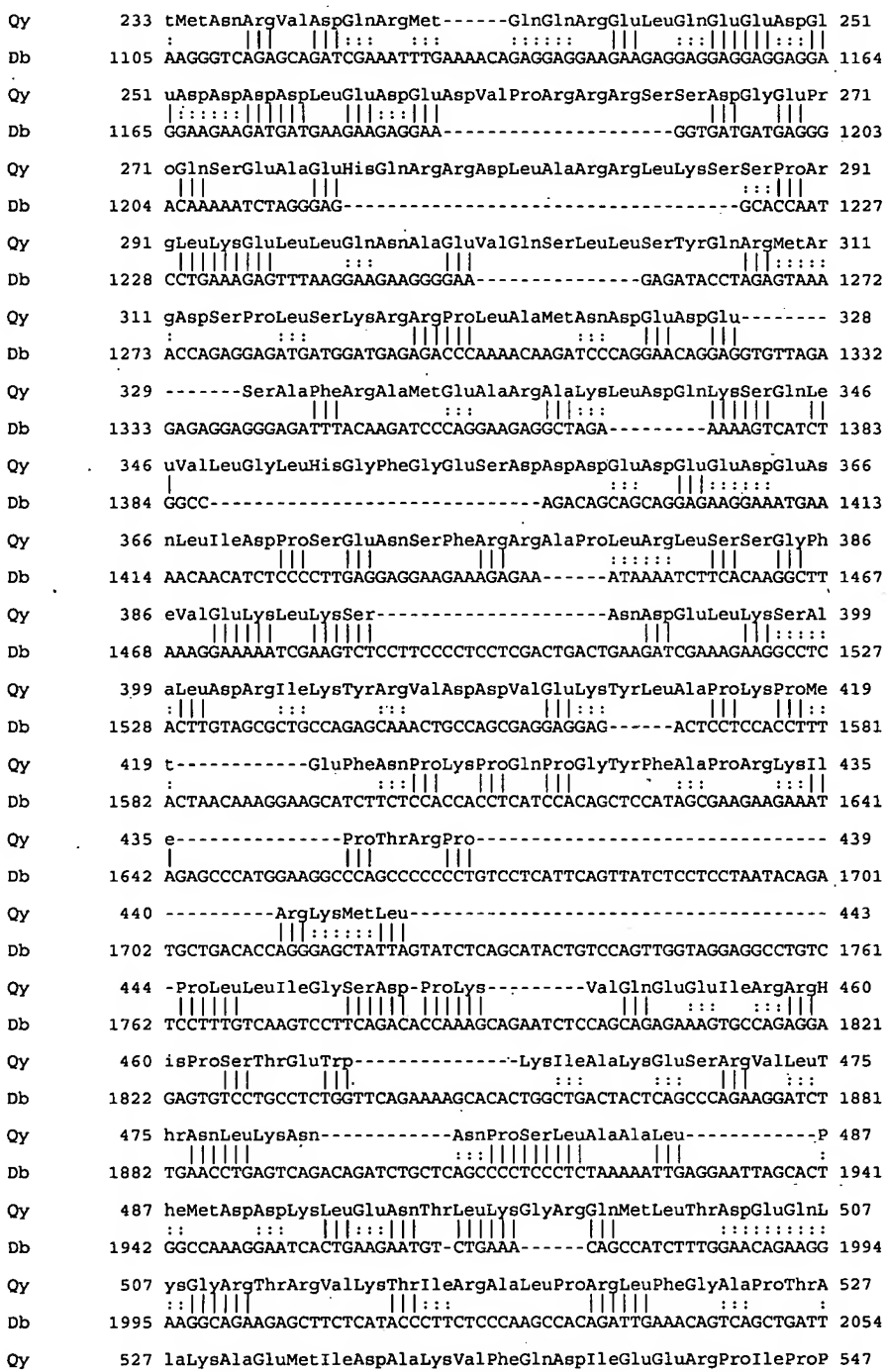

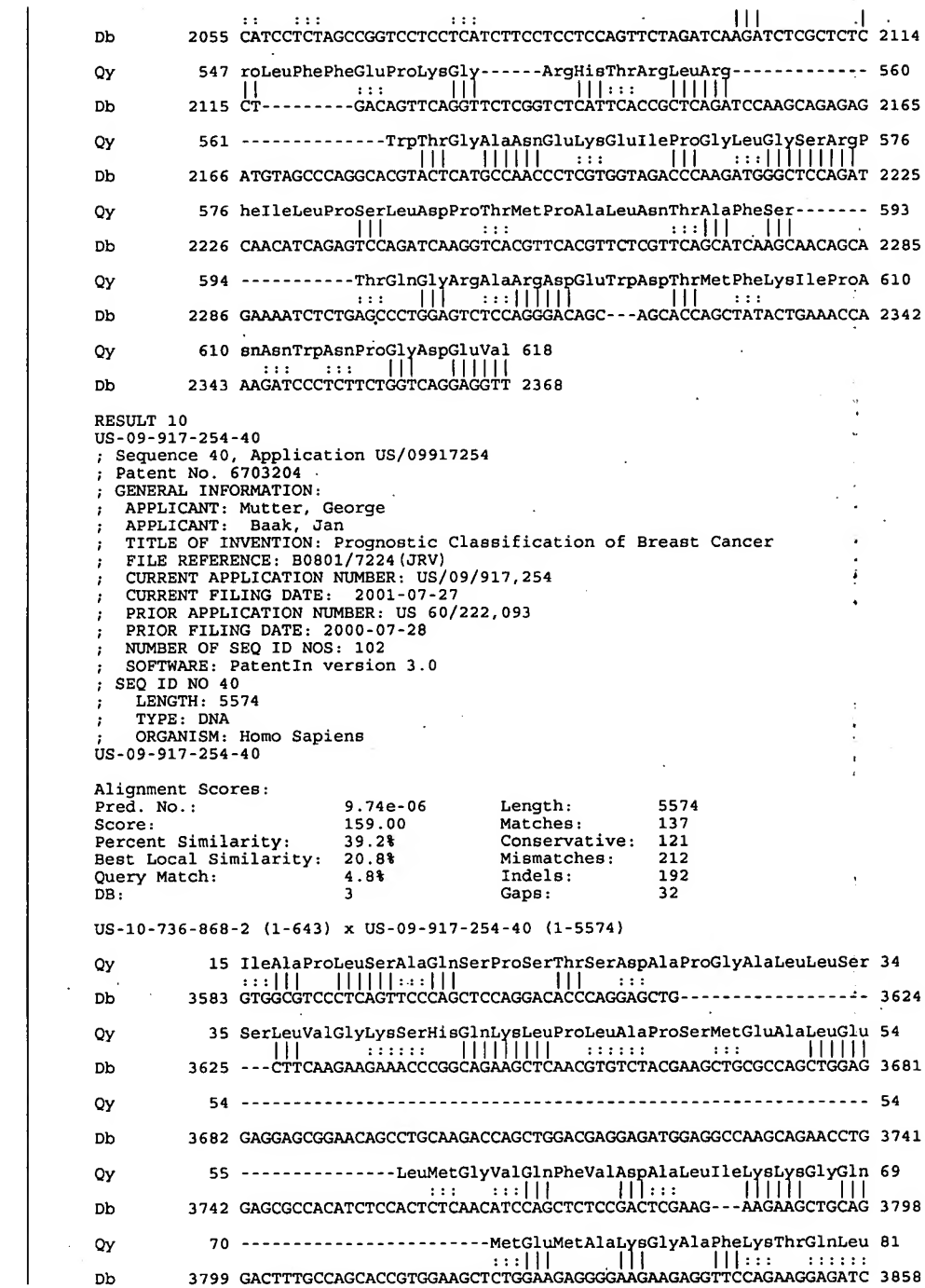

RESULT 10
US-09-917-254-40
; Sequence 40, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 5574
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-917-254-40

Alignment Scores:

Pred. No.:	9.74e-06	Length:	5574
Score:	159.00	Matches:	137
Percent Similarity:	39.2%	Conservative:	121
Best Local Similarity:	20.8%	Mismatches:	212
Query Match:	4.8%	Indels:	192
DB:	3	Gaps:	32

US-10-736-868-2 (1-643) x US-09-917-254-40 (1-5574)

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Qy        82 GluValLeuGluLysValHisProAspGln---------PheAspLysTyrLysLysLeu 98
Db      3859 GAGAACCTCACCCAGCAGTACGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACC 3918

Qy        99 Lys-----------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla 112
Db      3919 AAGAACAGGCTTCAGCAGGAGCTGGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA 3978

Qy       113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132
Db      3979 CTCGTGTCCAACCTGGAAAAGAAGCAGAGGAAA------TTTGATCAGTTGTTAGCCGAG 4032

Qy       133 GlyIleProIleGlySerSer---------------------------------------- 139
Db      4033 GAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCAGAAGCCAGG 4092

Qy       140 --------------------------IleArgGlyLeuGluAspAlaIleArgThrGln 150
Db      4093 GAGAAGGAAACCAAGGCCCTGTCCCTGGCTCGGGCCCTTGAAGAGGCCTTGGAAGCCAAA 4152

Qy       151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe 170
Db      4153 GAGGAACTCGAGCGGACCAAC---------AAAATGCTCAAAGCCGAAATGGAA------ 4197

Qy       171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189
Db      4198 ----------------------------GACCTGGTCAGCTCCAAGGATGACGTGGGC 4227

Qy       190 LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209
Db      4228 AAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGGCCCTGGAGACCCAGATGGAGGAGATG 4287

Qy       210 LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGlyGluGlu 229
Db      4288 AAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCACG-----------GAGGAC 4335

Qy       230 GlnArgMetMetMetAsnArgValAspGlnArgMetGln-----------------Gln 243
Db      4336 GCCAAACTG---------CGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCGAA 4386

Qy       244 ArgGluLeuGlnGluGluAspGluAspAspAspAspLeuGluAspGluAspValProArg 263
Db      4387 AGGGATCTCCAAGCCCGGGACGAGCAGAATGAG------GAGAAGAGGAGGCAACTGCAG 4440

Qy       264 ArgArgSerSerAspGlyGluProGlnSerGluAlaGluHisGlnArgArgAspLeuAla 283
Db      4441 AGACAGCTTCACGAGTATGAGACGGAACTGGAAGACGAGCGAAAGCAACGTGCCCTGGCA 4500

Qy       284 ArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsnAlaGluValGlnSer 303
Db      4501 GCTGCAGCAAAGAAG------AAGCTGGAAGGGGACCTGAAAGACCTGGAGCTTCAGGCC 4554

Qy       304 LeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgProLeu------ 321
Db      4555 ---GACTCTGCCATCAAGGGGAGGGAGGAAGCCATCAAGCAGCTACGCAAACTGCAGGCT 4611

Qy       322 AlaMetAsnAsp--------------GluAspGluSerAlaPheArg---AlaMetGlu 335
Db      4612 CAGATGAAGGACTTTCAAAGAGAGCTGGAAGATGCCCGTGCCTCCAGAGATGAGATCTTT 4671

Qy       336 AlaArgAlaLysLeuAspGlnLysSerGlnLeuValLeuGlyLeuHisGlyPheGlyGlu 355
Db      4672 GCCACAGCCAAAGAGAATGAGAAGAAAGCCAAGAGCTTG-----------------GAA 4713

Qy       356 SerAspAspAspGluAspGluGluAspGluAsnLeuIleAspProSerGluAsnSerPhe 375
Db      4714 GCAGACCTCATGCAGCTACAAGAGGAC---------CTCGCCGCCGCTGAGAGGGCTCGC 4764

Qy       376 ArgArgAlaProLeu---------ArgLeuSerSerGlyPheValGluLysLeuLysSer 392
Db      4765 AAACAAGCGGACCTCGAGAAGGAGGAACTGGCAGAGGAGCTGGCCAGTAGCCTGTCGGGA 4824

Qy       393 AsnAspGluLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAspValGluLys 412
Db      4825 AGGAACGCACTCCAGGACGAGAAGCGCCGCCTGGAGGCCCGGATCGCCCAGCTGGAGGAG 4884

Qy       413 TyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyrPheAlaPro 432
Db      4885 GAGCTGGAGGAGGAGCAGGG-CAACATGGAGGCCATGAGCGACCGGGTCC-GCAAAGCCA 4942

Qy       433 ArgLysIleProThr--------------------------------ArgProArgLys 441
Db      4943 CACAGCAGGCCGAGCAGCTCAGCAACGAGCTGGCCACAGAGCGCAGCACGGCCCAGAAGA 5002

Qy       442 Met---LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIleArgArgHis 460
Db      5003 ATGAGAGTGCCC---------GGCAGCAGCTCGAGCGGCAGAACAAGGAGCTCCGGAGCA 5053

Qy       461 ProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeuLysAsnAsn 480
Db      5054 AGCTCCACGAGATGGAGGGG-GCCGTCAAGTCC-----------------AAGTTCAAG 5094

Qy       481 ProSerLeuAlaAlaLeu--------------PheMetAspAspLysLeuGluAsnThr 495
Db      5095 TCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTCGAGCAGGAG 5154

Qy       496 LeuLysGlyArgGlnMetLeuThr----------------------------------- 503
Db      5155 GCCAGAGAGAAACAGGCGGCCACCAAGTCGCTGAAGCAGAAAGACAAGAAGCTGAAGGAA 5214

Qy       504 -----------------AspGlu---------------------------------Gln 506
Db      5215 ATCTTGCTGCAGGTGGAGGACGAGCGCAAGATGGCCGAGCAGTACAAGGAGCAGGCAGAG 5274

Qy       507 LysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGlyAlaProThr 526
Db      5275 AAAGGCAATGCCAGGGTCAAGCAGCTCAAG---------AGGCAGCTGGAGGAGGCAGAG 5325

Qy       527 AlaLysAlaGluMetIleAspAla---------LysValPheGlnAspIleGluGlu 542
Db      5326 GAGGAGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGAGCTGGATGAG 5382
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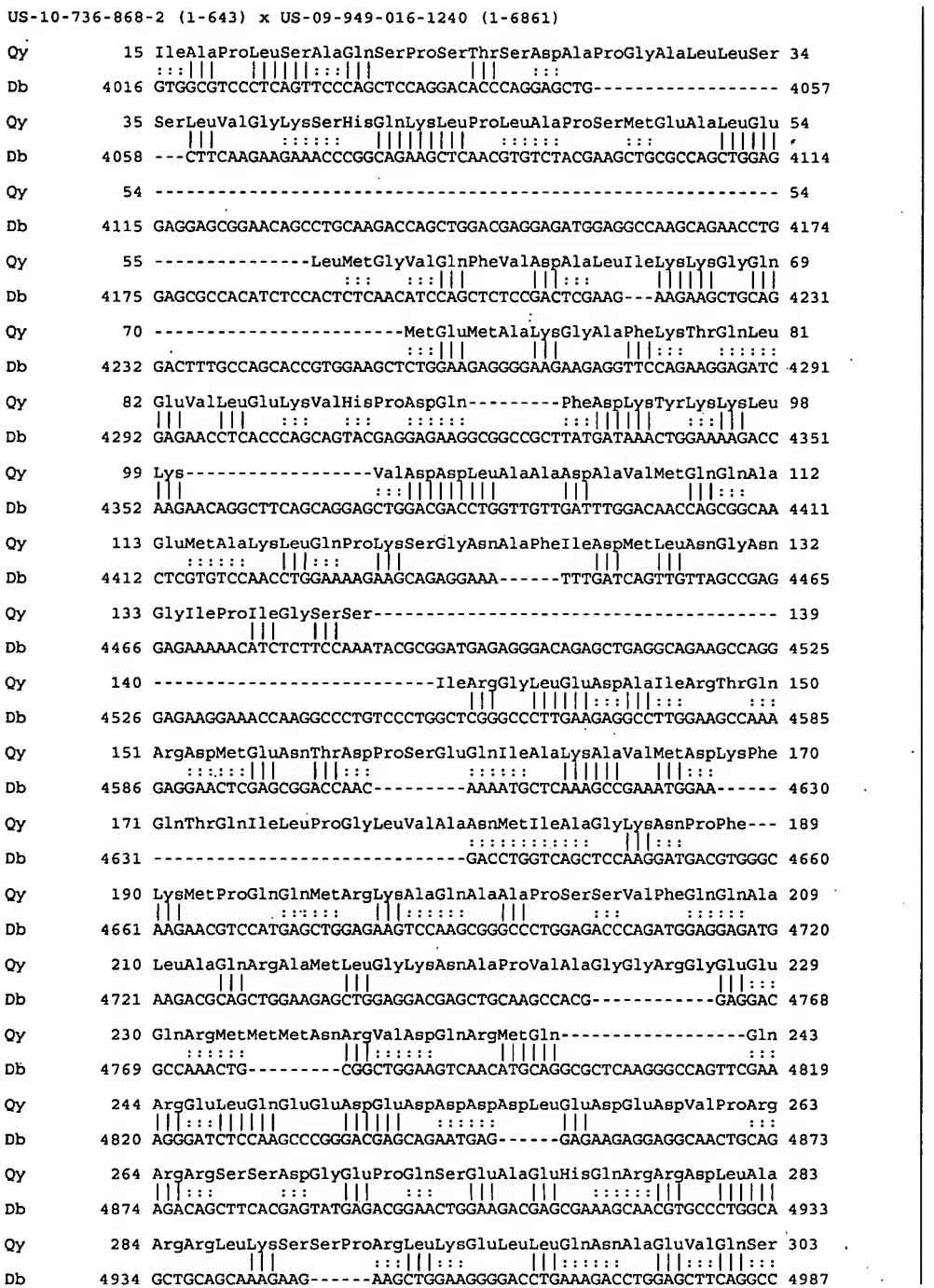
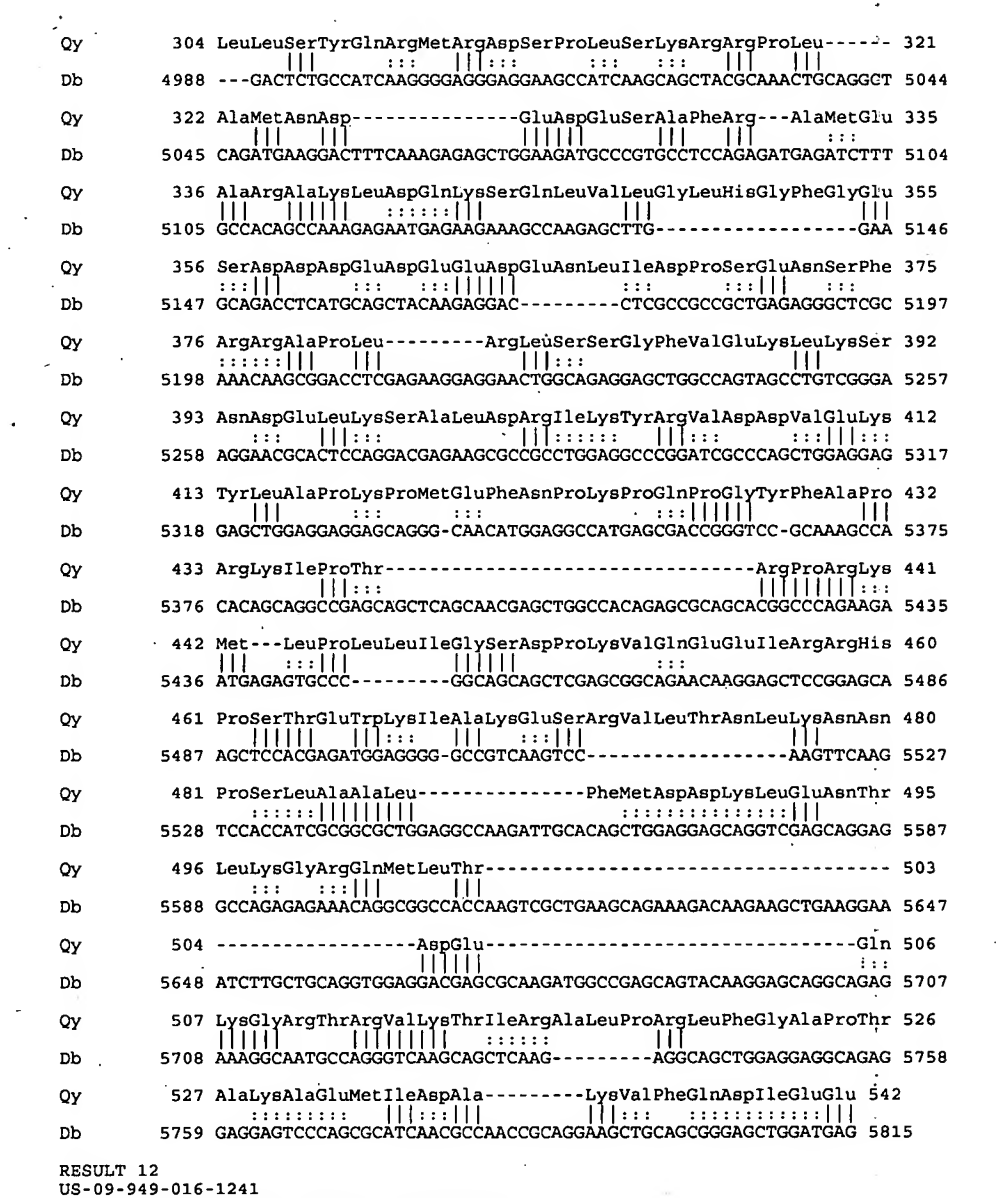
RESULT 11
US-09-949-016-1240
; Sequence 1240, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1240
; LENGTH: 6861
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1240

Alignment Scores:

Pred. No.:	1.35e-05	Length:	6861
Score:	159.00	Matches:	137
Percent Similarity:	39.2%	Conservative:	121
Best Local Similarity:	20.8%	Mismatches:	212
Query Match:	4.8%	Indels:	192
DB:	3	Gaps:	32

US-10-736-868-2 (1-643) x US-09-949-016-1240 (1-6861)





RESULT 12
US-09-949-016-1241
; Sequence 1241, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1241
;   LENGTH: 6861
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1241

Alignment Scores:
Pred. No.:                1.35e-05      Length:          6861
Score:                    159.00        Matches:         137
Percent Similarity:       39.2%         Conservative:    121
Best Local Similarity:    20.8%         Mismatches:      212
Query Match:              4.8%          Indels:          192
DB:                       3             Gaps:            32

US-10-736-868-2 (1-643) x US-09-949-016-1241 (1-6861)

Qy         15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaLeuLeuSer 34
              :::|||   ||||||:::|||         |||   :::
Db       4016 GTGGCGTCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGCTG------------------ 4057

Qy         35 SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu 54
                ||| :::::: |||||||||  ::::::     :::     ||||||
Db       4058 ---CTTCAAGAAGAAACCCGGCAGAAGCTCAACGTGTCTACGAAGCTGCGCCAGCTGGAG 4114

Qy         54 ------------------------------------------------------------ 54

Db       4115 GAGGAGCGGAACAGCCTGCAAGACCAGCTGGACGAGGAGATGGAGGCCAAGCAGAACCTG 4174

Qy         55 --------------LeuMetGlyValGlnPheValAspAlaLeuIleLysLysGlyGln 69
                           :::   :::|||      |||:::      ||||||   |||
Db       4175 GAGCGCCACATCTCCACTCTCAACATCCAGCTCTCCGACTCGAAG---AAGAAGCTGCAG 4231

Qy         70 ------------------------MetGluMetAlaLysGlyAlaPheLysThrGlnLeu 81
                                    :::|||     |||     |||:::   ::::::
Db       4232 GACTTTGCCAGCACCGTGGAAGCTCTGGAAGAGGGGAAGAAGAGGTTCCAGAAGGAGATC 4291

Qy         82 GluValLeuGluLysValHisProAspGln---------PheAspLysTyrLysLysLeu 98
              |||   |||   :::   :::   ::::::         :::||||||   :::|||
Db       4292 GAGAACCTCACCCAGCAGTACGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACC 4351

Qy         99 Lys------------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla 112
              |||                  :::||||||||||      |||          |||:::
Db       4352 AAGAACAGGCTTCAGCAGGAGCTGGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA 4411

Qy        113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132
              ::::::   |||:::   |||                |||   |||
Db       4412 CTCGTGTCCAACCTGGAAAAGAAGCAGAGGAAA------TTTGATCAGTTGTTAGCCGAG 4465

Qy        133 GlyIleProIleGlySerSer---------------------------------------- 139
                       |||   |||
Db       4466 GAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCAGAAGCCAGG 4525

Qy        140 --------------------------IleArgGlyLeuGluAspAlaIleArgThrGln 150
                                       |||   ||||||:::|||:::      :::
Db       4526 GAGAAGGAAACCAAGGCCCTGTCCCTGGCTCGGGCCCTTGAAGAGGCCTTGGAAGCCAAA 4585

Qy        151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe 170
              ::::::|||   |||:::         ::::::   ||||||   |||:::
Db       4586 GAGGAACTCGAGCGGACCAAC---------AAAATGCTCAAAGCCGAAATGGAA------ 4630

Qy        171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189
                                       :::::::::::   |||:::
Db       4631 ----------------------------GACCTGGTCAGCTCCAAGGATGACGTGGGC 4660

Qy        190 LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209
              |||         ::::::   |||::::::   |||      :::      ::::::

Db       4661 AAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGGCCCTGGAGACCCAGATGGAGGAGATG 4720

Qy        210 LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGlyGluGlu 229
                 |||         |||                                   |||:::
Db       4721 AAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCACG-----------GAGGAC 4768

Qy        230 GlnArgMetMetMetAsnArgValAspGlnArgMetGln----------------Gln 243
                 ::::::         |||::::::      ||||||                ::::
Db       4769 GCCAAACTG---------CGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCGAA 4819

Qy        244 ArgGluLeuGlnGluGluAspGluAspAspAspAspLeuGluAspGluAspValProArg 263
              |||:::||||||      ||||||  ::::::      |||                ::::
Db       4820 AGGGATCTCCAAGCCCGGGACGAGCAGAATGAG------GAGAAGAGGAGGCAACTGCAG 4873

Qy        264 ArgArgSerSerAspGlyGluProGlnSerGluAlaGluHisGlnArgArgAspLeuAla 283
              |||:::      :::   |||   :::   |||   |||   :::::::|||   ||||||
Db       4874 AGACAGCTTCACGAGTATGAGACGGAACTGGAAGACGAGCGAAAGCAACGTGCCCTGGCA 4933

Qy        284 ArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsnAlaGluValGlnSer 303
                    |||         :::|||:::      |||::::::   |||:::|||:::
Db       4934 GCTGCAGCAAAGAAG------AAGCTGGAAGGGGACCTGAAAGACCTGGAGCTTCAGGCC 4987

Qy        304 LeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgProLeu------ 321
                 |||      :::   |||:::      :::   :::   |||   |||
Db       4988 ---GACTCTGCCATCAAGGGGAGGGAGGAAGCCATCAAGCAGCTACGCAAACTGCAGGCT 5044

Qy        322 AlaMetAsnAsp--------------GluAspGluSerAlaPheArg---AlaMetGlu 335
                 |||   |||              ||||||      |||   |||      :::
Db       5045 CAGATGAAGGACTTTCAAAGAGAGCTGGAAGATGCCCGTGCCTCCAGAGATGAGATCTTT 5104

Qy        336 AlaArgAlaLysLeuAspGlnLysSerGlnLeuValLeuGlyLeuHisGlyPheGlyGlu 355
              |||   ||||||   ::::::|||          |||                  |||
Db       5105 GCCACAGCCAAAGAGAATGAGAAGAAAGCCAAGAGCTTG-----------------GAA 5146

Qy        356 SerAspAspAspGluAspGluGluAspGluAsnLeuIleAspProSerGluAsnSerPhe 375
              :::|||      :::   :::||||||         :::      :::|||   :::
Db       5147 GCAGACCTCATGCAGCTACAAGAGGAC---------CTCGCCGCCGCTGAGAGGGCTCGC 5197

Qy        376 ArgArgAlaProLeu---------ArgLeuSerSerGlyPheValGluLysLeuLysSer 392
              ::::::|||   |||            |||:::                  |||
Db       5198 AAACAAGCGGACCTCGAGAAGGAGGAACTGGCAGAGGAGCTGGCCAGTAGCCTGTCGGGA 5257

Qy        393 AsnAspGluLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAspValGluLys 412
              :::   |||:::         |||::::::   |||:::      :::|||:::
Db       5258 AGGAACGCACTCCAGGACGAGAAGCGCCGCCTGGAGGCCCGGATCGCCCAGCTGGAGGAG 5317

Qy        413 TyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyrPheAlaPro 432
                 |||      :::      :::          :::||||||          |||
Db       5318 GAGCTGGAGGAGGAGCAGGG-CAACATGGAGGCCATGAGCGACCGGGTCC-GCAAAGCCA 5375

Qy        433 ArgLysIleProThr--------------------------------ArgProArgLys 441
                 |||:::                                  |||||||||:::
Db       5376 CACAGCAGGCCGAGCAGCTCAGCAACGAGCTGGCCACAGAGCGCAGCACGGCCCAGAAGA 5435

Qy        442 Met---LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIleArgArgHis 460
              |||   :::|||         ||||||         :::
Db       5436 ATGAGAGTGCCC---------GGCAGCAGCTCGAGCGGCAGAACAAGGAGCTCCGGAGCA 5486

Qy        461 ProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeuLysAsnAsn 480
                 ||||||   |||:::   |||   :::|||                |||
Db       5487 AGCTCCACGAGATGGAGGGG-GCCGTCAAGTCC-----------------AAGTTCAAG 5527

Qy        481 ProSerLeuAlaAlaLeu--------------PheMetAspAspLysLeuGluAsnThr 495
                 ::::::|||||||||                    :::::::::::::::|||
Db       5528 TCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTCGAGCAGGAG 5587

Qy        496 LeuLysGlyArgGlnMetLeuThr---------------------------------- 503
                 :::   :::|||      |||
Db       5588 GCCAGAGAGAAACAGGCGGCCACCAAGTCGCTGAAGCAGAAAGACAAGAAGCTGAAGGAA 5647

Qy        504 -----------------AspGlu---------------------------------Gln 506
                              ||||||                                 :::
Db       5648 ATCTTGCTGCAGGTGGAGGACGAGCGCAAGATGGCCGAGCAGTACAAGGAGCAGGCAGAG 5707
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Qy       507 LysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGlyAlaProThr 526
Db      5708 AAAGGCAATGCCAGGGTCAAGCAGCTCAAG---------AGGCAGCTGGAGGAGGCAGAG 5758

Qy       527 AlaLysAlaGluMetIleAspAla---------LysValPheGlnAspIleGluGlu 542
Db      5759 GAGGAGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGAGCTGGATGAG 5815

RESULT 13
US-09-949-016-1242
; Sequence 1242, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1242
;   LENGTH: 6861
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1242

Alignment Scores:
Pred. No.:                1.35e-05      Length:          6861
Score:                    159.00        Matches:         137
Percent Similarity:       39.2%         Conservative:    121
Best Local Similarity:    20.8%         Mismatches:      212
Query Match:              4.8%          Indels:          192
DB:                       3             Gaps:            32

US-10-736-868-2 (1-643) x US-09-949-016-1242 (1-6861)

Qy        15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaLeuLeuSer 34
Db      4016 GTGGCGTCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGCTG---------------- 4057

Qy        35 SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu 54
Db      4058 ---CTTCAAGAAGAAACCCGGCAGAAGCTCAACGTGTCTACGAAGCTGCGCCAGCTGGAG 4114

Qy        54 ------------------------------------------------------------ 54
Db      4115 GAGGAGCGGAACAGCCTGCAAGACCAGCTGGACGAGGAGATGGAGGCCAAGCAGAACCTG 4174

Qy        55 --------------LeuMetGlyValGlnPheValAspAlaLeuIleLysLysGlyGln 69
Db      4175 GAGCGCCACATCTCCACTCTCAACATCCAGCTCTCCGACTCGAAG---AAGAAGCTGCAG 4231

Qy        70 ----------------------MetGluMetAlaLysGlyAlaPheLysThrGlnLeu 81
Db      4232 GACTTTGCCAGCACCGTGGAAGCTCTGGAAGAGGGGAAGAAGAGGTTCCAGAAGGAGATC 4291

Qy        82 GluValLeuGluLysValHisProAspGln---------PheAspLysTyrLysLysLeu 98
Db      4292 GAGAACCTCACCCAGCAGTACGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACC 4351

Qy        99 Lys-----------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla 112
Db      4352 AAGAACAGGCTTCAGCAGGAGCTGGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA 4411

Qy       113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132

Db      4412 CTCGTGTCCAACCTGGAAAAGAAGCAGAGGAAA------TTTGATCAGTTGTTAGCCGAG 4465

Qy       133 GlyIleProIleGlySerSer---------------------------------------- 139
Db      4466 GAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCAGAAGCCAGG 4525

Qy       140 --------------------------IleArgGlyLeuGluAspAlaIleArgThrGln 150
Db      4526 GAGAAGGAAACCAAGGCCCTGTCCCTGGCTCGGGCCCTTGAAGAGGCCTTGGAAGCCAAA 4585

Qy       151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe 170
Db      4586 GAGGAACTCGAGCGGACCAAC---------AAAATGCTCAAAGCCGAAATGGAA------ 4630

Qy       171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189
Db      4631 ----------------------------GACCTGGTCAGCTCCAAGGATGACGTGGGC 4660

Qy       190 LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209
Db      4661 AAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGGCCCTGGAGACCCAGATGGAGGAGATG 4720

Qy       210 LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGlyGluGlu 229
Db      4721 AAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCACG-----------GAGGAC 4768

Qy       230 GlnArgMetMetMetAsnArgValAspGlnArgMetGln-----------------Gln 243
Db      4769 GCCAAACTG---------CGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCGAA 4819

Qy       244 ArgGluLeuGlnGluGluAspGluAspAspAspAspLeuGluAspGluAspValProArg 263
Db      4820 AGGGATCTCCAAGCCCGGGACGAGCAGAATGAG------GAGAAGAGGAGGCAACTGCAG 4873

Qy       264 ArgArgSerSerAspGlyGluProGlnSerGluAlaGluHisGlnArgArgAspLeuAla 283
Db      4874 AGACAGCTTCACGAGTATGAGACGGAACTGGAAGACGAGCGAAAGCAACGTGCCCTGGCA 4933

Qy       284 ArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsnAlaGluValGlnSer 303
Db      4934 GCTGCAGCAAAGAAG------AAGCTGGAAGGGGACCTGAAAGACCTGGAGCTTCAGGCC 4987

Qy       304 LeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgProLeu------ 321
Db      4988 ---GACTCTGCCATCAAGGGGAGGGAGGAAGCCATCAAGCAGCTACGCAAACTGCAGGCT 5044

Qy       322 AlaMetAsnAsp--------------GluAspGluSerAlaPheArg---AlaMetGlu 335
Db      5045 CAGATGAAGGACTTTCAAAGAGAGCTGGAAGATGCCCGTGCCTCCAGAGATGAGATCTTT 5104

Qy       336 AlaArgAlaLysLeuAspGlnLysSerGlnLeuValLeuGlyLeuHisGlyPheGlyGlu 355
Db      5105 GCCACAGCCAAAGAGAATGAGAAGAAAGCCAAGAGCTTG-----------------GAA 5146

Qy       356 SerAspAspAspGluAspGluGluAspGluAsnLeuIleAspProSerGluAsnSerPhe 375
Db      5147 GCAGACCTCATGCAGCTACAAGAGGAC---------CTCGCCGCCGCTGAGAGGGCTCGC 5197

Qy       376 ArgArgAlaProLeu---------ArgLeuSerSerGlyPheValGluLysLeuLysSer 392
Db      5198 AAACAAGCGGACCTCGAGAAGGAGGAACTGGCAGAGGAGCTGGCCAGTAGCCTGTCGGGA 5257

Qy       393 AsnAspGluLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAspValGluLys 412
Db      5258 AGGAACGCACTCCAGGACGAGAAGCGCCGCCTGGAGGCCCGGATCGCCCAGCTGGAGGAG 5317

Qy       413 TyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyrPheAlaPro 432
Db      5318 GAGCTGGAGGAGGAGCAGGG-CAACATGGAGGCCATGAGCGACCGGGTCC-GCAAAGCCA 5375

Qy       433 ArgLysIleProThr--------------------------------ArgProArgLys 441
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Db       5376 CACAGCAGGCCGAGCAGCTCAGCAACGAGCTGGCCACAGAGCGCAGCACGGCCCAGAAGA 5435

Qy        442 Met---LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIleArgArgHis 460
              |||   :::|||         ||||||             :::
Db       5436 ATGAGAGTGCCC---------GGCAGCAGCTCGAGCGGCAGAACAAGGAGCTCCGGAGCA 5486

Qy        461 ProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeuLysAsnAsn 480
              ||||||   |||:::   |||   :::|||                  |||
Db       5487 AGCTCCACGAGATGGAGGGG-GCCGTCAAGTCC-----------------AAGTTCAAG 5527

Qy        481 ProSerLeuAlaAlaLeu---------------PheMetAspAspLysLeuGluAsnThr 495
              :::::|||||||||                 :::::::::::::::|||
Db       5528 TCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTCGAGCAGGAG 5587

Qy        496 LeuLysGlyArgGlnMetLeuThr---------------------------------- 503
              :::   :::|||      |||
Db       5588 GCCAGAGAGAAACAGGCGGCCACCAAGTCGCTGAAGCAGAAAGACAAGAAGCTGAAGGAA 5647

Qy        504 -----------------AspGlu---------------------------------Gln 506
                              ||||||                                 :::
Db       5648 ATCTTGCTGCAGGTGGAGGACGAGCGCAAGATGGCCGAGCAGTACAAGGAGCAGGCAGAG 5707

Qy        507 LysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGlyAlaProThr 526
              ||||||    ||||||||   ::::::        |||
Db       5708 AAAGGCAATGCCAGGGTCAAGCAGCTCAAG---------AGGCAGCTGGAGGAGGCAGAG 5758

Qy        527 AlaLysAlaGluMetIleAspAla---------LysValPheGlnAspIleGluGlu 542
              :::::::::   |||:::|||         |||:::   ::::::::::::|||
Db       5759 GAGGAGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGAGCTGGATGAG 5815

RESULT 14
US-09-902-540-1175/c
; Sequence 1175, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1175
;   LENGTH: 19269
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-1175

Alignment Scores:
Pred. No.:              7.73e-05      Length:         19269
Score:                  158.50        Matches:        125
Percent Similarity:     37.3%         Conservative:   106
Best Local Similarity:  20.2%         Mismatches:     215
Query Match:            4.8%          Indels:         173
DB:                     3             Gaps:           29

US-10-736-868-2 (1-643) x US-09-902-540-1175 (1-19269)

Qy         27 AspAlaProGlyAlaLeuLeuSerSerLeuValGlyLysSerHisGlnLysLeuProLeu 46
              |||         ::::::|||             |||         ::::::      |||
Db      12884 GACGACGCCAGTAGCGTCCTGGATGAGTGGACGGGGAGTCGGTTCGAGCGG------CTC 12831

Qy         47 AlaProSerMetGluAlaLeuGluLeuMetGlyValGlnPheVal-------------- 61
              |||   |||   ||||||      |||:::          |||
Db      12830 GCTGAATCGCAGGAGGCGGATGCGTTGCTCCGAGGCTTCCTTGTCTCCAGCGTGCCCGGC 12771

Qy         62 AspAlaLeuIleLysLysGlyGlnMetGluMetAlaLysGlyAlaPheLysThrGlnLeu 81
              :::   :::   |||   |||         :::|||:::      :::      |||
Db      12770 AACGGCGTGACGAAGGTGGGCAACTGGGGCTTGGCTCGGTTGCTCTGGTTGAATCAGTCG 12711

Qy         82 GluValLeuGluLysValHisProAspGlnPheAspLysTyrLysLysLeuLysValAsp 101
              |||       |||:::                  |||       |||   ::::::
Db      12710 GAA------GAGCGGTACGACCTGCCCGGCCTCGATACACCGCTCAAGGCCCGCCTCCTT 12657

Qy        102 AspLeuAlaAlaAspAlaValMetGlnGlnAlaGluMetAlaLysLeuGln--------- 118
              :::           |||   :::         |||   :::   |||:::
Db      12656 GAGACGGTTGGAGTCGCCGCCCTGAGCAACGAGGAACAGTCCCTCCTGAAGGCAATGGAG 12597

Qy        119 ------------------------ProLysSerGlyAsnAlaPheIleAspMetLeuAsn 130
                                       ||||||:::|||               ::::::
Db      12596 GGGGCCTACCGCCAGTTCTTCACGCCCAAGACGGGAAAG-----------CTCGTCACC 12549

Qy        131 GlyAsnGlyIlePro---IleGlySerSerIleArgGlyLeu---GluAspAlaIleArg 148
              |||:::   :::         |||:::   :::|||   |||   |||:::|||   |||
Db      12548 GGAAGCGACCTCGATCGTGAGGGTGCTCGCATGCGGGAGTTGCGCGAGGAGGCAGCTCGG 12489

Qy        149 ---ThrGlnArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMet 167
                 |||||||||       |||                 ||||||:::|||          |||
Db      12488 TTGACTCAGCGGTTGGCGGAG-----------ATCGAGCAGCTTGCCAGCGAGAGCATG 12441

Qy        168 AspLysPheGlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsn 187
              |||       |||   |||:::
Db      12440 GACCTCGGCCAGAAGCAGCTC------------------------------------ 12420

Qy        188 ProPheLysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGln 207
                       :::   ::::::   |||     :::          :::|||:::   |||
Db      12419 ------TCCCTGGCGGAGGAACGGAGGACCTATGAGCAGCGGCTCGCTAGCTTG---CAG 12369

Qy        208 GlnAlaLeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGly 227
              :::   :::|||:::         |||   :::   |||   :::
Db      12368 GAGCGCATCGCGGAGGAGGAGAAGCTGGAGCAGCAGGCGGCGCTCCGGGAGAAGGACGTC 12309

Qy        228 GluGluGlnArgMetMetMetAsnArgValAspGlnArg-----------------Met 241
              |||   ||||||                :::||||||:::                :::
Db      12308 GAGCGTCAGCGAAAAGAGTGGCAGGCGCTGGACCAGAAGCAGCGAGAGCTTCTCGCGCTC 12249

Qy        242 GlnGlnArgGluLeuGlnGluGluAsp---------GluAspAspAspAspLeuGluAsp 258
              ||||||:::   :::|||:::||||||          ::::::          |||::::::
Db      12248 CAGCAGAAGGTGGTCCAGCAGGAGGACCTGCTGGCTCGCAACGAGCCGGCCTTGCAGGAG 12189

Qy        259 GluAspValProArgArgArgSerSerAspGlyGluProGlnSerGluAlaGluHisGln 278
                        ||||||:::   ||||||       ::::::          |||:::
Db      12188 GCCCAGGGACTCGTCCGGCGCGCCGAAGACGGGGCTCGCGAAGCACGCGAGCGACACAAG 12129

Qy        279 ArgArgAspLeuAlaArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsn 298
                                                                     |||
Db      12128 ------------------------------------------------GCTCAGCAG 12120

Qy        299 AlaGluValGlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArg 318
              ||||||:::      |||:::   ||||||:::          |||   :::
Db      12119 GGGGAGGTGGAG------CTGGCGGAGCAGCGCGTGGAACGAGGACGACTCCTCGAA--- 12069

Qy        319 ArgProLeuAlaMetAsnAspGluAspGluSerAlaPheArgAlaMetGluAlaArgAla 338
                                                          :::|||||||||
Db      12068 ------------------------------------------------GATGCGCGCGCT 12057

Qy        339 LysLeuAspGlnLysSerGlnLeuValLeuGlyLeuHisGlyPheGlyGluSerAspAsp 358
              |||   ::::::   :::|||
Db      12056 TCCCTGGCGGAGCAGCGGAAGTTG---------------------------------- 12033

Qy        359 AspGluAspGluGluAspGluAsnLeuIleAspProSerGluAsnSerPheArgArgAla 378
              |||         :::                 ::::::   :::      :::   ||||||
Db      12032 GACGGGCTCGTCAAGCAGGGGACGCGGGTGGAGACCGCAGTGGAGAATGCCCGACGCAAG 11973

Qy        379 ProLeuArgLeuSerSerGlyPheValGluLysLeuLysSerAsnAspGlu--------- 395
                    |||   :::             ::::::|||       :::|||
Db      11972 ACTGCGGCGCTGAAGGCGCTTCCAGACGCAGAGGTAAAGCGCGCCGAGGAGGTGCAGCGC 11913

Qy        396 ---LeuLysSerAlaLeuAspArgIleLysTyrArgValAspAspValGluLysTyrLeu 414
                 |||       ||||||||||:::         :::      :::|||      :::
Db      11912 AAGCTGAATCAGGCCCTGGACAGGCTGGACGCACAGGGGGTCGAGGTC---TCCTTCACT 11856
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Qy        415 AlaProLysProMetGluPheAsnProLysProGlnProGlyTyrPheAlaProArgLys 434
              |||     |||           :::    |||   |||:::       |||  .|||
Db      11855 GCCGAGAGCCCGCAGCGTATCGAGTGGGAGGCCCAG---GGTCACACCACACCGCACAAG 11799

Qy        435 IleProThrArgProArgLysMetLeuProLeuLeu---------------------- 446
              :::           :::|||:::        :::
Db      11798 CTCACAAGGGAGGAGCAGAAGGTCTTCTCGGGGGTGCGTGCTGGTGCACTGCGCATCAAG 11739

Qy        447 ------------------------------------IleGlySerAspProLysVal 453
                                                   ||||||        |||:::
Db      11738 GGAGTGGGTGAAGTCCGCGTGCGCACTGCGGCCGAGGAGATTGGC---------AAGCTC 11688

Qy        454 GlnGluGluIleArgArgHisProSer------------------------------- 462
              :::   |||:::   :::|||
Db      11687 GAAGCGGAGGTCGAGAAGCACCGGAAGGACCTGGCGCGCCGCCTCCATGAGCACGGAGTC 11628

Qy        463 --------------------ThrGluTrpLysIleAlaLysGluSerArgValLeuThr 475
                                  ||||||      |||   :::      ||||||
Db      11627 GATGATGTGGTGGGTCTGCGCGCGGAGTGG------GCGTCCCAGCAGGTCGTGCTTCAG 11574

Qy        476 AsnLeuLysAsnAsnProSerLeuAlaAlaLeuPheMetAspAspLysLeuGluAsnThr 495
              |||           :::   |||::::::|||          |||
Db      11573 GAGCTGTCGAAGTACGAGGAGGCACGGAGCCAGTTCTTGGAGGAC---------AACAAA 11523

Qy        496 LeuLysGlyArgGlnMetLeuThrAspGluGlnLysGlyArgThrArgValLysThrIle 515
              ::::::      :::::::|||   ::::::|||:::   :::   |||   ||||||
Db      11522 GTCGAGAGCGTCGAGGTGCTCAAGGAACAGCAGCGTGAGCAGGCACGG---AAGACG--- 11469

Qy        516 ArgAlaLeuProArgLeuPheGlyAlaProThrAlaLysAlaGluMetIleAspAlaLys 535
                                  ||||||   :::|||:::      :::
Db      11468 --------------------GGGGCACTGAGCGCCCAGCTCAACCTTTCGCGG------ 11436

Qy        536 ValPheGlnAspIleGluGluArgProIlePro---------ProLeuPhePheGluPro 552
                :::::::::::::     |||   |||           |||      |||
Db      11435 ------GAGGAGCTACAGACCCACCCATTTCCCGAGCTGAAGGCGCTGACGGAGGAACTC 11382

Qy        553 LysGlyArgHisThrArgLeuArgTrpThrGlyAlaAsnGluLysGluIleProGly 571
              |||   |||           ::::::           :::|||:::   |||
Db      11381 AAGGCCCGCAGGCAGGAGGTGAAGGCCCGGGACAAGGCGCGGGAGGAGGTGGAAGGA 11325

RESULT 15
US-08-875-435B-1
; Sequence 1, Application US/08875435B
; Patent No. 6593304
; GENERAL INFORMATION:
;  APPLICANT: Hasegawa, Kazuhide
;  APPLICANT:  Arakawa, Emi
;  APPLICANT:  Oda, Shoji
;  APPLICANT:  Matsuda, Yuzuru
;  APPLICANT:  Takahashi, Katsuhito
;  APPLICANT:  Sugahara, Michihiro
;  APPLICANT:  Ishiyama, Haruo
;  TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
;  TITLE OF INVENTION:  FOR MYOSIN HEAVY CHAIN SM1 ISOFORM PROTEIN INSERTED INTO
;  TITLE OF INVENTION:  VECTOR DNA, MICROORGANSIM CARRYING THE RECOMBINANT DNA, AND
;  TITLE OF INVENTION:  AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING THE
;  TITLE OF INVENTION:  RECOMBINANT DNA
;  FILE REFERENCE: 07898-013001
;  CURRENT APPLICATION NUMBER: US/08/875,435B
;  CURRENT FILING DATE:  1997-07-25
;  PRIOR APPLICATION NUMBER: PCT/JP96/00134
;  PRIOR FILING DATE: 1996-01-25
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 6175
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (105)...(6020)
US-08-875-435B-1
```

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Alignment Scores:
Pred. No.:              1.86e-05        Length:         6175
Score:                  157.00          Matches:        127
Percent Similarity:     38.3%           Conservative:   127
Best Local Similarity:  19.2%           Mismatches:     211
Query Match:            4.8%            Indels:         198
DB:                     3               Gaps:           32

US-10-736-868-2 (1-643) x US-08-875-435B-1 (1-6175)

Qy         15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaLeuLeuSer 34
              :::|||   |||   :::|||           |||   :::
Db       4032 GTGGCTTCCCTTGGATCCCAGCTTCAGGACACCCAAGAGCTG----------------- 4073

Qy         35 SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu 54
                |||     ::::::   |||||||||   ::::::      :::      ||||||
Db       4074 ---CTCCAAGAAGAAACCCGGCAGAAGCTCAATGTGTCTACCAAGCTGCGTCAGTTGGAA 4130

Qy         54 ------------------------------------------------------------ 54

Db       4131 GATGAAAGGAACAGCCTGCAGGACCAGCTGGATGAGGAGATGGAGGCTAAGCAAAACCTG 4190

Qy         55 --------------LeuMetGlyValGlnPheValAspAlaLeuIleLysLysGlyGln 69
                           :::   :::|||      |||:::      ||||||   |||
Db       4191 GAGCGCCATGTCTCAACACTGAACATTCAGCTCTCAGACTCTAAG---AAGAAGCTGCAG 4247

Qy         70 ----------------------MetGluMetAlaLysGlyAlaPheLysThrGlnLeu 81
                                    ||||||      |||         :::   ::::::
Db       4248 GACTTTGCAAGTACCATCGAGGTCATGGAGGAGGGGAAGAAGAGGTTACAGAAAGAGATG 4307

Qy         82 GluValLeuGluLysValHisProAspGln---------PheAspLysTyrLysLysLeu 98
              |||   |||  :::   :::   ::::::         :::||||||   ::|||
Db       4308 GAGGGCCTCAGCCAGCAGTATGAGGAGAAGGCGGCTGCCTATGACAAACTGGAGAAAACC 4367

Qy         99 Lys------------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla 112
              |||                 :::||||||||||      |||          |||:::
Db       4368 AAGAACAGGCTCCAGCAGGAGCTGGATGACCTGGTCGTGGACTTGGACAACCAGCGGCAA 4427

Qy        113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132
              ::::::  |||:::  |||                  |||   |||
Db       4428 CTGGTATCCAATCTGGAAAAGAAGCAGAAGAAA------TTTGACCAGTTGTTAGCTGAG 4481

Qy        133 GlyIleProIleGlySerSer---------------------------------------- 139
                  |||  |||
Db       4482 GAGAAGAACATCTCCTCCAAGTATGCGGATGAGAGAGACCGAGCTGAAGCAGAGGCCAGG 4541

Qy        140 --------------------------IleArgGlyLeuGluAspAlaIleArgThrGln 150
                                       |||   ||||||:::|||:::      :::
Db       4542 GAAAAGGAGACAAAGGCTTTGTCTCTAGCCCGGGCCCTGGAGGAAGCCCTGGAAGCCAAA 4601

Qy        151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe 170
              ::::::|||   |||:::        ::::::  ||||||   |||:::
Db       4602 GAAGAGCTGGAGAGGACCAAC---------AAGATGCTCAAAGCTGAGATGGAA------ 4646

Qy        171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMet---IleAlaGlyLysAsnProPhe 189
                                  ||||||::::::           |||||||||
Db       4647 -----------------GACCTGGTCAGCTCCAAGGATGATGTAGGCAAGAACGTGCAT 4688

Qy        190 LysMetProGlnGlnMetArg-------------------------LysAlaGlnAla 200
              ::::::   :::      |||                       |||   |||
Db       4689 GAACTGGAGAAGTCCAAGCGTGCCTTGGAGACCCAGATGGAAGAGATGAAAACCCAGCTG 4748

Qy        201 AlaProSerSerValPheGlnGlnAlaLeuAlaGlnArgAlaMetLeuGlyLysAsnAla 220
                 |||          ||||||     :::   |||   |||
Db       4749 GAGGAGTCGGAGGATGACGTGCAGGCC---ACTGAGGATGCCAAGCTGCGGCTAGAGGTC 4805

Qy        221 ProValAlaGlyGlyArgGlyGluGluGlnArgMetMetMetAsnArgValAspGlnArg 240
              :::          :::|||:::   :::|||   :::       |||   :::|||
Db       4806 AACATGCAGGCCCTCAAGGGCCAGTTTGAACGCGATCTCCAGGCTCGGGATGAACAGAAT 4865

Qy        241 MetGln---GlnArgGluLeuGlnGluGlu---AspGluAspAspAspAspLeuGluAsp 258
              :::  :::|||:::||||||   :::      |||   :::   :::|||||||||
Db       4866 GAGGAGAAGAGGAGGCAGCTACAGCGGCAGCTGCACGAGTATGAGACAGAACTGGAAGAT 4925
```

```
Qy       259 GluAspValProArgArgArgSerSerAspGlyGluProGlnSerGluAlaGluHisGln 278
             |||         ::::::|||:::           :::   :::   |||
Db      4926 GAA------CGGAAGCAGAGAGCTCTGGCGGCGGCAGCTAAGAAGAAGCTGGAAGGGGAC 4979

Qy       279 ArgArgAspLeuAlaArgArgLeuLysSerSerProArgLeuLysGlu------LeuLeu 296
               :::|||||||      :::      |||:::   :::   :::|||      :::
Db      4980 CTAAAAGACCTAGAGCTCCAGGCTGACTCAGCCATCAAAGGGAGGGAGGAAGCCATCAAG 5039

Qy       297 GlnAsnAlaGluValGlnSer---LeuLeuSerTyrGlnArg---MetArgAspSerPro 314
             |||.     ::::::|||:::   :::      :::||||||   :::   |||:::
Db      5040 CAGCTTCGAAAACTGCAGGCTCAGATGAAGGACTTCCAAAGAGAGCTGGATGATGCCCGT 5099

Qy       315 LeuSerLysArgArgProLeuAlaMetAsnAspGluAspGluSerAlaPheArgAlaMet 334
               |||:::          |||   :::   |||:::|||          :::::::::
Db      5100 GCCTCCAGGGATGAGATCTTTGCCACCTCAAAAGAGAATGAGAAGAAAGCCAAGAGTCTG 5159

Qy       335 GluAla-------------------------------------------------Arg 337
             ||||||                                                 :::
Db      5160 GAGGCAGACCTCATGCAGCTCCAAGAGGACCTGGCAGCAGCTGAGAGAGCTCGCAAGCAA 5219

Qy       338 AlaLysLeuAspGlnLys---------SerGlnLeuValLeuGlyLeuHisGlyPheGly 354
             |||   |||:::::::::           :::|||          |||   |||
Db      5220 GCTGACCTGGAGAAGGAGGAGCTGGCCGAGGAGCTGGCTAGCAGCTTGTCAGGAAGGAAT 5279

Qy       355 GluSerAspAsp-----------------------------------------AspGluAsp 361
                 |||                                               :::|||
Db      5280 ACACTGCAGGATGAGAAGCGCCGCCTGGAGGCAAGGATCGCCCAACTAGAGGAGGAGCTG 5339

Qy       362 GluGluAspGluAsnLeuIleAspProSerGluAsnSerPheArgArgAlaProLeu--- 380
             ||||||::::::      ::::::          :::      |||:::|||   |||
Db      5340 GAGGAAGAGCAGGGCAACATGGAGGCCATGAGTGATAGAGTACGCAAGGCCACACTGCAG 5399

Qy       381 ------ArgLeuSerSerGlyPheValGluLys---------LeuLysSerAsnAspGlu 395
                 :::||||||:::           :::            :::   |||:::
Db      5400 GCTGAGCAACTGAGCAATGAGCTGGCCACAGAACGCAGCACGGCTCAGAAGAATGAGAGC 5459

Qy       396 LeuLysSerAlaLeuAspArg------------IleLysTyrArgValAspAspValGlu 411
                :::      |||:::|||           ::::::   ::::::   :::||||||
Db      5460 GCACGGCAACAGCTGGAGCGCCAGAACAAGGAACTGCGAAGCAAGTTGCAGGAGGTAGAA 5519

Qy       412 LysTyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyrPheAla 431

Db      5519 ------------------------------------------------------------ 5519

Qy       432 ProArgLysIleProThrArgProArgLysMetLeuProLeuLeuIleGlySerAspPro 451
                    :::      :::   :::      :::      |||
Db      5520 ---GGTGCTGTCAAAGCCAAGCTCAAGTCCACTGTTGCGGCGCTGGAGGCCAAGATTGCA 5576

Qy       452 LysValGlnGluGluIleArgArgHisProSerThrGluTrpLysIleAlaLysGluSer 471
             :::::::::|||::::::   :::                        |||:::|||
Db      5577 CAGCTGGAGGAGCAGGTTGAACAGGAG--------------------GCCAGAGAGAAA 5615

Qy       472 ArgValLeuThr---AsnLeuLysAsnAsnProSerLeuAlaAlaLeuPheMetAspAsp 490
             :::      |||   :::||||||                              |||
Db      5616 CAGGCGGCCACCAAGTCGCTGAAGCAAAAG----------------------GACAAG 5651

Qy       491 LysLeuGluAsnThrLeu----------------------LysGlyArgGlnMetLeu 502
             ||||||:::      |||                          |||
Db      5652 AAGCTAAAGGAGGTCCTGCTGCAGGTGGAGGATGAGCGCAAGATGGCAGAGCAGTACAAG 5711

Qy       503 ThrAspGluGlnLysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPhe 522
                :::||||||   |||:::||||||   ::::::         |||
Db      5712 GAGCAGGCAGAGAAAGGAAACACCAAGGTCAAGCAGCTGAAG---------AGGCAGCTG 5762

Qy       523 GlyAlaProThrAlaLysAlaGluMetIleAspAla---------LysValPheGlnAsp 539
                         :::::::::   |||:::|||          |||:::   ::::::
Db      5763 GAAGAGGCAGAGGAGGAGTCCCAGTGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGAG 5822

Qy       540 IleGluGlu 542
             :::::::|||
Db      5823 CTAGATGAG 5831
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Search completed: March 3, 2006, 18:41:26
Job time : 462 secs